

1/54

FIG. 1

1 AAAATGTATG GATACAACTT ACGTTTGATG AAAGATTGG GCTTGAAGAC CCAGAAGATG
 TTTTACATAC CTATGTTGAA TGCAAACTAC TTTCTAAACC CGAACTTCTG GGTCTTCTAC

 61 ACATATGCAA GTATGATTTT GTAGAAGTTG AGGAACCCAG TGATGGAAC ATATTAGGGC
 TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC ACTACCTTGA TATAATCCCC

 121 GCTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTC TAAAGGAAAT CAAATTAGGA
 CGACCACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG ATTCCTTTA GTTTAATCCT

 +1 MetAsn IlePheLeu LeuAsnLeuLeu ThrGluGlu ValArgLeu
 }-----
 181 TAAGATTTGT ATCTGATGAA TATTTTCCTT CTGAACCTTC TAACAGAGGA GGTAAGATTA
 ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGGAAG ATTGTCTCCT CCATTCTAAT

 +1 TyrSerCysThr ProArgAsn PheSerVal SerIleArgGlu GluLeuLys ArgThrAsp

 241 TACAGCTGCA CACCTCGTAA CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT
 ATGTGCGACGT GTGGAGCATT GAAGAGTCAC AGGTATTCCC TTCTTGATTT CTCTTGCTA

 +1 ThrIlePheTrp ProGlyCys LeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys

 301 ACCATTTTCT GGCCAGGTTG TCTCCTGGTT AAACGCTGTG GTGGGAACTG TGCCTGTGTG
 TGGTAAAAGA CCGGTCCAAC AGAGGACCAA TTTGCGACAC CACCTTGAC ACGGACAACA

 +1 LeuHisAsnCys AsnGluCys GlnCysVal ProSerLysVal ThrLysLys TyrHisGlu

 361 CTCCACAATT GCAATGAATG TCAATGTGTC CCAAGCAAAG TTAATAAAAA ATACCACGAG
 GAGGTGTTAA CGTTACTTAC AGTTACACAG GGTTCGTTTC AATGATTTTT TATGGTGCTC

 +1 ValLeuGlnLeu ArgProLys ThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal

 421 GTCCTTCAGT TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG
 CAGGAAGTCA ACTCTGGTTT CTGGCCACAG TCCCCTAACG TGTTTAGTGA GTGGCTGCAC

 +1 AlaLeuGluHis HisGluGlu CysAspCys ValCysArgGly SerThrGly Gly
 ----->
 481 GCCCTGGAGC ACCATGAGGA GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCCG
 CGGGACCTCG TGGTACTCCT CACACTGACA CACACGTCTC CCTCGTGTCC TCCTATCGGC

 541 CATCACCACC AGCAGCTCTT GCCCAGAGCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA
 GTAGTGGTGG TCGTCGAGAA CGGGTCTCGA CACGTACAGT CACCGACTAA GATAATCTCT

 601 ACGTATGCGT TATCTCCATC CTTAATCTCA GTTGTGTTGCT TCAAGGACCT TTCATCTTCA
 TGCATACGCA ATAGAGGTAG GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT

 661 GGATTTACAG TGCATTCTGA AAGAGGAGAC ATCAAACAGA ATTAGGAGTT GTGCAACAGC
 CCTAAATGTC ACGTAAGACT TTCTCCTCTG TAGTTGTCT TAATCCTCAA CACGTTGTGC

 721 TCTTTTGA GAAGGCCTAA AGGACAGGAG AAAAGGTCTT CAATCGTGGA AAGAAAATTA
 AGAAAACCTCT CCTCCGATT TCCTGTCCTC TTTTCCAGAA GTTAGCACCT TTCTTTTAAT

 781 AATGTTGTAT TAAATAGATC ACCAGCTAGT TTCAGAGTTA CCATGTACGT ATTCCACTAG
 TTACAACATA ATTTATCTAG TGGTCGATCA AAGTCTCAAT GGTACATGCA TAAGGTGATC

2/54

FIG. 1 (CONTINUED).

841 CTGGGTTCTG TATTTCAGTT CTTTCGATAC GGCTTAGGGT AATGTCAGTA CAGGAAAAAA
 GACCCAAGAC ATAAAGTCAA GAAAGCTATG CCGAATCCCA TTACAGTCAT GTCCTTTTTT

 901 ACTGTGCAAG TGAGCACCTG ATTCCGTTGC CTTGCTTAAC TCTAAAGCTC CATGTCCTGG
 TGACACGTTT ACTCGTGGAC TAAGGCAACG GAACGAATTG AGATTTTCGAG GTACAGGACC

 961 GCCTAAAATC GTATAAAATC TGGATTTTTT TTTTTTTTTT TGCTCATATT CACATATGTA
 CGGATTTTAG CATATTTTAG ACCTAAAAAA AAAAAAAAAA ACGAGTATAA GTGTATACAT

 1021 AACCAGAACA TTCTATGTAC TACAAACCTG GTTTTTAAAA AGGAACTATG TTGCTATGAA
 TTGGTCTTGT AAGATACATG ATGTTTGGAC CAAAAATTTT TCCTTGATAC AACGATACTT

 1081 TTAAACTTGT GTCGTGCTGA TAGGACAGAC TGGATTTTTT ATATTTCTTA TTAAATTTTC
 AATTTGAACA CAGCACCAGT ATCCTGTCTG ACCTAAAAAG TATAAGAAT AATTTTAAAG

 1141 TGCCATTTAG AAGAAGAGAA CTACATTCAT GGTTCGGAAG AGATAAACCT GAAAAGAAGA
 ACGGTAAATC TTCTTCTCTT GATGTAAGTA CCAAACCTTC TCTATTTGGA CTTTCTTCT

 1201 GTGGCCTTAT CTTCACTTTA TCGATAAGTC AGTTTATTTG TTTCAATTGTG TACATTTTTA
 CACCGGAATA GAAGTGAAAT AGCTATTCAG TCAAATAAAC AAAGTAACAC ATGTAAAAAT

 1261 TATTCTCCTT TTGACATTAT AACTGTTGGC TTTTCTAATC TTGTTAAATA TATCTATTTT
 ATAAGAGGAA AACTGTAATA TTGACAACCG AAAAGATTAG AACAATTTAT ATAGATAAAA

 1321 TACCAAAGGT ATTTAATATT CTTTTTTATG ACAACTTAGA TCAACTATTT TTAGCTTGGT
 ATGGTTTCCA TAAATTATAA GAAAAAATAC TGTGAATCT AGTTGATAAA AATCGAACCA

 1381 AAATTTTTCT AAACACAATT GTTATAGCCA GAGGAACAAA GATGATATAA AATATTGTTG
 TTTAAAAAGA TTTGTGTAA CAATATCGGT CTCCTTGTTT CTACTATATT TTATAACAAC

 1441 CTCTGACAAA AATACATGTA TTTCAATCTC GTATGGTGCT AGAGTTAGAT TAATCTGCAT
 GAGACTGTTT TTATGTACAT AAAGTAAGAG CATAACACGA TCTCAATCTA ATTAGACGTA

 1501 TTTAAAAAAC TGAATTGGAA TAGAATTGGT AAGTTGCAAA GACTTTTTGA AAATAATTAA
 AAATTTTTTG ACTTAACCTT ATCTTAACCA TTCAACGTTT CTGAAAACT TTTATTAATT

 1561 ATTATCATAT CTCCATTCC TGTTATTGGA GATGAAAATA AAAAGCAACT TATGAAAGTA
 TAATAGTATA GAAGGTAAGG ACAATAACCT CTACTTTTAT TTTTCGTTGA ATACTTTCAT

 1621 GACATTCAGA TCCAGCCATT ACTAACCTAT TCCTTTTTTG GGGAAATCTG AGCCTAGCTC
 CTGTAAGTCT AGGTCGGTAA TGATTGGATA AGGAAAAAAC CCCTTTAGAC TCGGATCGAG

 1681 AGAAAAACAT AAAGCACCTT GAAAAAGACT TGGCAGCTTC CTGATAAAGC GTGCTGTGCT
 TCTTTTGTGA TTTCGTGGA CTTTTTCTGA ACCGTGGAAG GACTATTTCT CACGACACGA

 1741 GTGCAGTAGG AACACATCCT ATTTATTGTG ATGTTGTGGT TTTATTATCT TAAACTCTGT
 CACGTCATCC TTGTGTAGGA TAAATAACAC TACAACACCA AAATAATAGA ATTTGAGACA

 1801 TCCATACACT TGTATAAATA CATGGATATT TTTATGTACA GAAGTATGTC TCTTAACCAG
 AGGTATGTGA ACATATTTAT GTACCTATAA AAATACATGT CTTCATACAG AGAATTGGTC

 1861 TTCACTTATT GTACCTGG
 AAGTGAATAA CATGGACC

3/54

FIG. 2. Predicted VEGF-like protein encoded by Incyte contig of 8/12/98

1 MNIFLLNLLT EEVRLYSCTP RNFSVSIREE LKRTDTIFWP GCLLVKRCGG
51 NCACCLHNCN ECQCVPSKVT KKYHEVLQLR PKTGVRGLHK SLTDVALEHH
101 EECDCVCRGS TGG

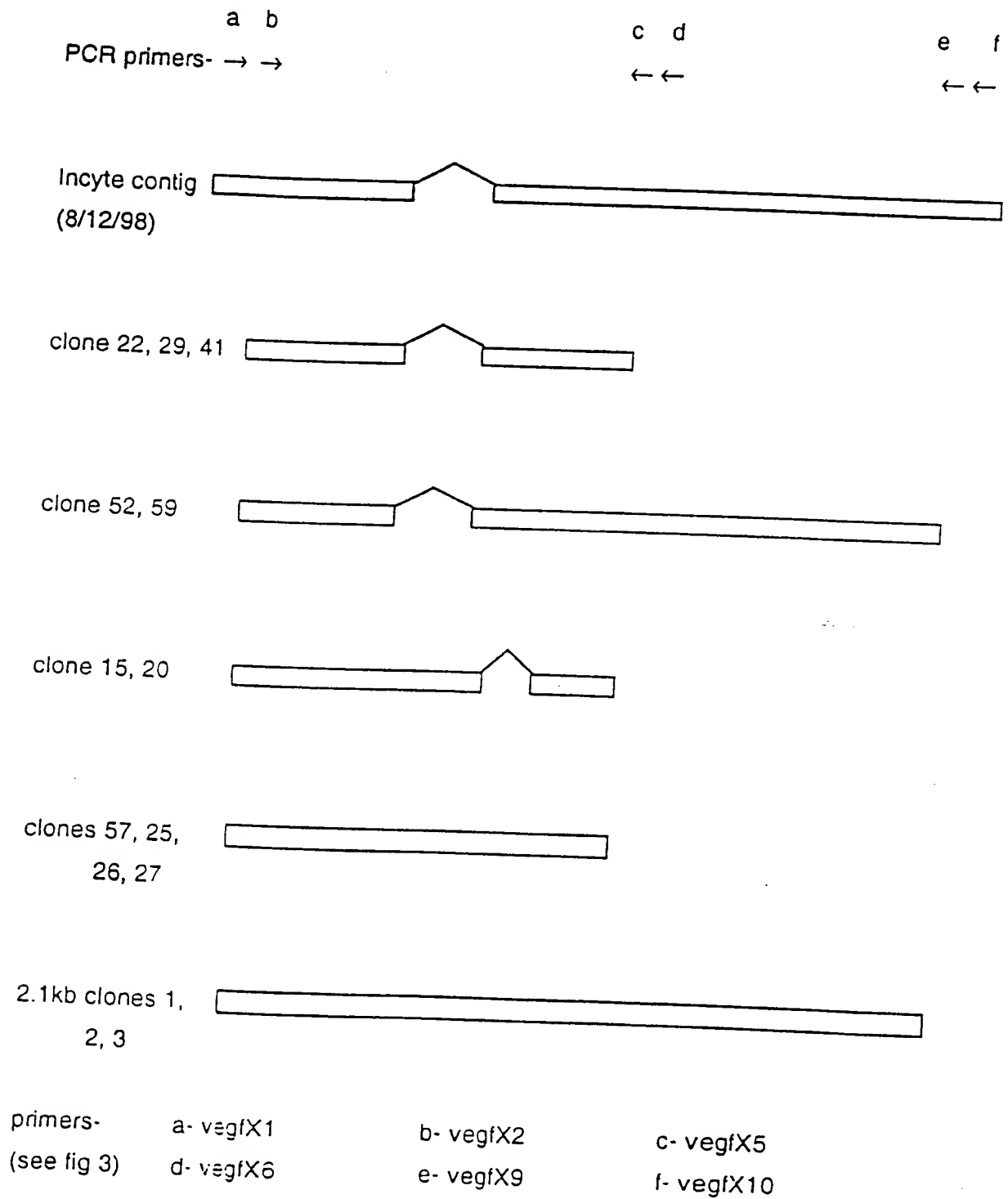
FIG. 3. PCR primers for cloning VEGF-X

vegX1	AAAATGTATGGATACAACTTAC
vegX2	GTTTGATGAAAGATTGTTGGGCTTG
vegX3	TTTCTAAAGGAAATCAAATTAG
vegX4	GATAAGATTTGTATCTGATG
vegX5	GATGTCTCCTCTTTCAG
vegX6	GCACAACTCCTAATTCTG
vegX7	AGCACCTGATTCCGTTGC
vegX8	TAGTACATAGAATGTTCTGG
vegX9	AAGAGACATACTTCTGTAC
vegX10	CCAGGTACAATAAGTGAACTG

FIG. 4.

4/54

Variants Isolated by PCR (at 8/2/99, all cloned and sequenced at



5/54

FIG. 5. VEGF-X 5' RACE primers

vegX11	CCTTTAGAAATCTGTTTTCCTGGTACAG
vegX12	GGAAAATATTCATCAGATACAAATCTTATCC
vegX13	GGTCCAGTGGCAAAGCTGAAGG
vegX14	CTGGTTCAAGATATCGAATAAGGTCTTCC

6/54

FIG. 6. DNA sequence assembled from in-house clones and 5'RACE

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1  TGCCAGAGCA GGTGGGCGCT TCCACCCCG TGCAGCCTTC CCCTGGCGGT GGTGAAAGAG
   ACGGTCTCGT CCACCCGCGA AGGTGGGGTC ACGTCGGAAG GGGACCGCCA CCACTTTCTC

61  ACTCGGGAGT CGCTGCTTCC AAAGTGCCCG CCGTGAGTGA GCTCTCACCC CAGTCAGCCA
   TGAGCCCTCA GCGACGAAGG TTTCACGGGC GGCACCTACT CGAGAGTGGG GTCAGTCCGT

+2  MetSerLeu PheGlyLeuLeu LeuLeuThr SerAlaLeu AlaGlyGlnArg GlnGlyTh
   }-----
121  AATGAGCCTC TTCGGGCTTC TCCTGCTGAC ATCTGCCCTG GCCGGCCAGA GACAGGGGAC
   TTACTCGGAG AAGCCCGAAG AGGACGACTG TAGACGGGAC CGGCCGGTCT CTGTCCCCTG

+2  rGlnAlaGlu SerAsnLeuSer SerLysPhe GlnPheSer SerAsnLysGlu GlnAsnGl
   -----
181  TCAGGCGGAA TCCAACCTGA GTAGTAAATT CCAGTTTTC AGCAACAAGG AACAGAACGG
   AGTCCGCCTT AGGTGGACT CATCATTTAA GGTCAAAAGG TCGTTGTTC TTGTCTTGCC

+2  yValGlnAsp ProGlnHisGlu ArgIleIle ThrValSer ThrAsnGlySer IleHisSe
   -----
241  AGTACAAGAT CCTCAGCATG AGAGAATTAT TACTGTGTCT ACTAATGGAA GTATTCACAG
   TCATGTTCTA GGAGTCGTAC TCTCTTAATA ATGACACAGA TGATTACCTT CATAAGTGTC

+2  rProArgPhe ProHisThrTyr ProArgAsn ThrValLeu ValTrpArgLeu ValAlaVa
   -----
301  CCCAAGGTTT CCTCATACTT ATCCAAGAAA TACGGTCTTG GTATGGAGAT TAGTAGCAGT
   GGGTTCCAAA GGAGTATGAA TAGGTTCTTT ATGCCAGAAC CATACCTCTA ATCATCGTCA

+2  lGluGluAsn ValTrpIleGln LeuThrPhe AspGluArg PheGlyLeuGlu AspProGl
   -----
361  AGAGGAAAT GTATGGATAC AACTTACCTT TGATGAAAGA TTTGGGCTTG AAGACCCAGA
   TCTCCTTTTA CATACCTATG TTGAATGCAA ACTACTTTCT AAACCCGAAC TTCTGGGTCT

+2  uAspAspIle CysLysTyrAsp PheValGlu ValGluGlu ProSerAspGly ThrIleLe
   -----
421  AGATGACATA TGCAAGTATG ATTTTGTAGA AGTTGAGGAA CCCAGTGATG GAACTATATT
   TCTACTGTAT ACGTTCATAC TAAAACATCT TCAACTCCTT GGGTCACTAC CTTGATATAA

+2  uGlyArgTrp CysGlySerGly ThrValPro GlyLysGln IleSerLysGly AsnGlnIl
   -----
481  AGGGCGCTGG TGTGGTTCTG TACTGTACC AGGAAAACAG ATTTCTAAAG GAAATCAAAT
   TCCCGCGACC ACACCAAGAC CATGACATGG TCCTTTTGTC TAAAGATTTC CTTTAGTTTA

+2  eArgIleArg PheValSerAsp GluTyrPhe ProSerGlu ProGlyPheCys IleHisTy
   -----
541  TAGGATAAGA TTTGTATCTG ATGAATATTT TCCTTCTGAA CCAGGGTTCT GCATCCACTA
   ATCCTATTCT AACATAGAC TACTTATAAA AGGAAGACTT GGTCCCAAGA CGTAGGTGAT

+2  rAsnIleVal MetProGlnPhe ThrGluAla ValSerPro SerValLeuPro ProSerAl
   -----
601  CAACATTGTC ATGCCACAAT TCACAGAAGC TGTGAGTCTT TCACTGCTAC CCGCTTCAGC
   GTTGTAACAG TACGGTGTTA AGTGTCTTCC AACTCAAGG AGTCACGATG GGGGAAGTCG

+2  aLeuProLeu AspLeuLeuAsn AsnAlaIle ThrAlaPhe SerThrLeuGlu AspLeuIl
   -----
661  TTTGCCACTG GACCTGCTTA ATAATGCTAT AACTGCCTTT AGTACCTTGG AAGACCTTAT
   AAACGGTGAC CTGGACGAAT TATTACGATA TTGACGGAAA TCATCGAACC TTCTCGAATA

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7/54

FIG. 6 (CONTINUED 1).

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+2 eArgTyrLeu GluProGluArg TrpGlnLeu AspLeuGlu AspLeuTyrArg ProThrTr
-----
721 TCGATATCTT GAACCAGAGA GATGGCAGTT GGACTTAGAA GATCTATATA GGCCAACTTG
    AGCTATAGAA CTTGGTCTCT CTACCGTCAA CCTGAATCTT CTAGATATAT CCGGTTGAAC

+2 pGlnLeuLeu GlyLysAlaPhe ValPheGly ArgLysSer ArgValValAsp LeuAsnLe
-----
781 GCAACTTCTT GGCAAGGCTT TTGTTTTTGG AAGAAAATCC AGAGTGGTGG ATCTGAACCT
    CGTTGAAGAA CCGTTCCGAA AACAAAAACC TTCTTTTAGG TCTCACCACC TAGACTTGGA

+2 uLeuThrGlu GluValArgLeu TyrSerCys ThrProArg AsnPheSerVal SerIleAr
-----
841 TCTAACAGAG GAGGTAAGAT TATACAGCTG CACACCTCGT AACTTCTCAG TGTCCATAAG
    AGATTGTCTC CTCCATTCTA ATATGTCGAC GTGTGGAGCA TTGAAGAGTC ACAGGTATTC

+2 gGluGluLeu LysArgThrAsp ThrIlePhe TrpProGly CysLeuLeuVal LysArgCy
-----
901 GGAAGAACTA AAGAGAACCG ATACCATTTT CTGGCCAGGT TGTCTCCTGG TTAAACGCTG
    CCTCTTGAT TTCTCTTGGC TATGGTAAAA GACCGGTCCA ACAGAGGACC AATTTGCGAC

+2 sGlyGlyAsn CysAlaCysCys LeuHisAsn CysAsnGlu CysGlnCysVal ProSerLy
-----
961 TGGTGGGAAC TGTGCCTGTT GTCTCCACAA TTGCAATGAA TGTCAATGTG TCCAAGCAA
    ACCACCCTTG ACACGGACAA CAGAGGTGTT AACGTTACTT ACAGTTACAC AGGGTTCGTT

+2 sValThrLys LysTyrHisGlu ValLeuGln LeuArgPro LysThrGlyVal ArgGlyLe
-----
1021 AGTTACTAAA AAATACCACG AGGTCCTTCA GTTGAGACCA AAGACCGGTG TCAGGGGATT
    TCAATGATTT TTTATGGTGC TCCAGGAAGT CAACTCTGGT TTCTGGCCAC AGTCCCCTAA

+2 uHisLysSer LeuThrAspVal AlaLeuGlu HisHisGlu GluCysAspCys ValCysAr
-----
1081 GCACAAATCA CTCACCGACG TGGCCCTGGA GCACCATGAG GAGTGTGACT GTGTGTGCAG
    CGTGTTTAGT GAGTGGCTGC ACCGGGACCT CGTGGTACTC CTCACACTGA CACACACGTC

+2 gGlySerThr GlyGly
----->
1141 AGGGAGCACA GGAGGATAGC CGCATCACCA CCAGCAGCTC TTGCCCAGAG CTGTGCAGTG
    TCCCTCGTGT CCTCCTATCG GCGTAGTGGT GGTGTCGAG AACGGGTCTC GACACGTCAC

1201 CAGTGGCTGA TTCTATTAGA GAACGTATGC GTTATCTCCA TCCTTAATCT CAGTTGTTTG
    GTCACCGACT AAGATAATCT CTTGCATACG CAATAGAGGT AGGAATTAGA GTCAACAAAC

1261 CTTCAAGGAC CTTTCATCTT CAGGATTTAC AGTGCATTCT GAAAGAGGAG ACATCAAACA
    GAAGTTCTCTG GAAAGTAGAA GTCCTAAATG TCACGTAAGA CTTTCTCCTC TGTAGTTTGT

1321 GAATTAGGAG TTGTGCAACA GCTCTTTTGA GAGGAGGCCT AAAGGACAGG AGAAAAGGTC
    CTTAATCCTC AACACGTTGT CGAGAAAAC CTCTCCCGA TTTCTGTCC TCTTTTCCAG

1381 TTCAATCGTG GAAAGAAAAT TAAATGTTGT ATTAAATAGA TCACCAGCTA GTTTCAGAGT
    AAGTTAGCAC CTTTCTTTTA ATTTACAACA TAATTTATCT AGTGGTCGAT CAAAGTCTCA

1441 TACCATGTAC GTATTCCACT AGCTGGGTTT TGTATTTTCTG TTCTTTTCGAT ACGGCTTAGG
    ATGGTACATG CATAAGGTGA TCGACCCAAG ACATAAAGTC AAGAAAGCTA TGCCGAATCC

1501 GTAATGTCAG TACAGGAAAA AAAGTGTGCA AGTGAGCACC TGATTCCGTT GCCTTGCTTA
    CATTACAGTC ATGTCCTTTT TTTGACACGT TCACTCGTGG ACTAAGGCAA CGGAACGAAT

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8/54

FIG. 6 (CONTINUED 2).

1561 ACTCTAAAGC TCCATGTCCT GGGCCTAAAA TCGTATAAAA TCTGGATTTT TTTTTTTTTT
 TGAGATTTTC AGGTACAGGA CCCGGATTTT AGCATATTTT AGACCTAAAA AAAAAAAAAA
 1621 TTTGCTCATA TTCACATATG TAAACCAGAA CATTCTATGT ACTACAAACC TGGTTTTTAA
 AAACGAGTAT AAGTGTATAC ATTTGGTCTT GTAAGATACA TGATGTTTGG ACCAAAAATT
 1681 AAAGGAACTA TGTGCTATG AATTAACTT GTGTCGTGCT GATAGGACAG ACTGGATTTT
 TTTCTTGAT ACAACGATAC TTAATTTGAA CACAGCACGA CTATCCTGTC TGACCTAAAA
 1741 TCATATTTCT TATTAATAATT TCTGCCATTT AGAAGAAGAG AACTACATTC ATGGTTTGA
 AGTATAAAGA ATAATTTTAA AGACGGTAAA TCTTCTTCTC TTGATGTAAG TACCAAACCT
 1801 AGAGATAAAC CTGAAAAGAA GAGTGGCCTT ATCTTCACTT TATCGATAAG CCAGTTTATT
 TCTCTATTTG GACTTTTCTT CTCACCGGAA TAGAAGTGAA ATAGCTATTC GGTCAAATAA
 1861 TGTTTCATTG TGTACATTTT TATATTCTCC TTTTGACATT ATAAGTGTG GCTTTTCTAA
 ACAAAGTAAC ACATGTAAAA ATATAAGAGG AAAACTGTAA TATTGACAAC CGAAAAGATT
 1921 TCTTGTTAAA TATATCTATT TTTACCAAAG GTATTTAATA TTCTTTTTTA TGACAACTTA
 AGAACAATTT ATATAGATAA AAATGGTTTC CATAAATTAT AAGAAAAAAT ACTGTTGAAT
 1981 GATCAACTAT TTTTAGCTTG GTAAATTTTT CTAAACACAA TTGTTATAGC CAGAGGAACA
 CTAGTTGATA AAAATCGAAC CATTTAAAAA GATTGTGTG AACAATATCG GTCTCCTTGT
 2041 AAGATGATAT AAAATATTGT TGCTCTGACA AAAATACATG TATTTTATTTC TCGTATGGTG
 TTCTACTATA TTTTATAACA ACGAGACTGT TTTTATGTAC ATAAAGTAAG AGCATACCAC
 2101 CTAGAGTTAG ATTAATCTGC ATTTTAAAAA ACTGAATTGG AATAGAATTG GTAAGTTGCA
 GATCTCAATC TAATTAGACG TAAAATTTTT TGACTTAACC TTATCTTAAC CATTCAACGT
 2161 AAGACTTTTT GAAAATAATT AAATTATCAT ATCTTCCATT CCTGTTATTG GAGATGAAAA
 TTCTGAAAAA CTTTTATTAA TTTAATAGTA TAGAAGGTAA GGACAATAAC CTCTACTTTT
 2221 TAAAAAGCAA CTTATGAAAG TAGACATTCA GATCCAGCCA TTACTAACCT ATTCCTTTTT
 ATTTTTCGTT GAATACTTTC ATCTGTAAGT CTAGGTCGGT AATGATTGGA TAAGGAAAAA
 2281 TGGGGAAATC TGAGCCTAGC TCAGAAAAAC ATAAAGCACC TTGAAAAAGA CTGGCAGCT
 ACCCCTTTAG ACTCGGATCG AGTCTTTTGT TATTTCTGTG AACTTTTTCT GAACCGTCGA
 2341 TCCTGATAAA GCGTGCTGTG CTGTGCAGTA GGAACACATC CTATTTATTG TGATGTTGTG
 AGGACTATTT CGCACGACAC GACACGTCAT CCTTGTGTAG GATAAATAAC ACTACAACAC
 2401 GTTTTATTAT CTTAACTCT GTTCCATACA CTTGTATAAA TACATGGATA TTTTATGTA
 CAAAATAATA GAATTTGAGA CAAGGTATGT GAACATATTT ATGTACCTAT AAAAATACAT
 2461 CAGAAGTATG TCTCT
 GTCTTCATAC AGAGA

9/54

FIG. 7.

New Sequence + Incyte ESTs

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1  ATTTGTTTAA ACCTTGGGAA ACTGGTTCAG GTCCAGGTTT TGCTTTGATC CTTTTCAAAA
   TAAACAAATT TGGAACCCTT TGACCAAGTC CAGGTCCAAA ACGAAACTAG GAAAAGTTTT

61  ACTGGAGACA CAGAAGAGGG CTTCTAGGAA AAAGTTTTGG GATGGGATTA TGTGGAAACT
   TGACCTCTGT GTCTTCTCCC GAAGATCCTT TTTCAAACC CTACCCTAAT ACACCTTTGA

121  ACCCTGCGAT TCTCTGCTGC CAGAGCAGGC TCGGCGCTTC CACCCAGTG CAGCCTTCCC
   TGGGACGCTA AGAGACGACG GTCTCGTCCG AGCCGCGAAG GTGGGGTCAC GTCGGAAGGG

181  CTGGCGGTGG TGAAAGAGAC TCGGGAGTCG CTGCTTCCAA AGTGCCCGCC GTGAGTGAGC
   GACCGCCACC ACTTCTCTG AGCCCTCAGC GACGAAGGTT TCACGGGCGG CACTCACTCG

+2                                     Met SerLeuPhe GlyLeuLeu LeuLeuThrSer AlaLeuAl
   ]-----

241  TCTCACCCCA GTCAGCCAAA TGAGCCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC
   AGAGTGGGGT CAGTCGGTTT ACTCGGAGAA GCCCGAAGAG GACGACTGTA GACGGGACCG

+2  aGlyGlnArg GlnGlyThrGln AlaGluSer AsnLeuSer SerLysPheGln PheSerSe
   -----

301  CGGCCAGAGA CAGGGGACTC AGGCGGAATC CAACCTGAGT AGTAAATTCC AGTTTTCAG
   GCCGTCTCT GTCCCTGAG TCCGCCTTAG GTTGGACTCA TCATTAAAGG TCAAAGGTC

+2  rAsnLysGlu GlnTyrGlyVal GlnAspPro GlnHisGlu ArgIleIleThr ValSerTh
   -----

361  CAACAAGGAA CAGTACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA CTGTGTCTAC
   GTTGTTCCTT GTCATGCCTC ATGTTCTAGG AGTCGTACTC TCTTAATAAT GACACAGATG

+2  rAsnGlySer IleHisSerPro ArgPhePro HisThrTyr ProArgAsnThr ValLeuVa
   -----

421  TAATGGAAGT ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA CGGTCTTGGT
   ATTACCTTCA TAAGTGTCGG GTTCCAAAGG AGTATGAATA GGTCTTTTAT GCCAGAACCA

+2  lTrpArgLeu ValAlaValGlu GluAsnVal TrpIleGln LeuThrPheAsp GluArgPh
   -----

481  ATGGAGATTA GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG ATGAAAGATT
   TACCTCTAAT CATCGTCATC TCCTTTTACA TACCTATGTT GAATGCAAAC TACTTTCTAA

+2  eGlyLeuGlu AspProGluAsp AspIleCys LysTyrAsp PheValGluVal GluGluPr
   -----

541  TGGGCTTGAA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG TTGAGGAACC
   ACCCGAACTT CTGGGTCTTC TACTGTATAC GTTCATACTA AAACATCTTC AACTCCTTGG

+2  oSerAspGly ThrIleLeuGly ArgTrpCys GlySerGly ThrValProGly LysGlnIl
   -----

601  CAGTGATGGA ACTATATTAG GGCGCTGGTG TGGTTCTGGT ACTGTACCAG GAAAACAGAT
   GTCACTACCT TGATATAATC CCGCGACCAC ACCAAGACCA TGACATGGTC CTTTGTCTA

+2  eSerLysGly AsnGlnIleArg IleArgPhe ValSerAsp GluTyrPhePro SerGluPr
   -----

661  TTCTAAAGGA AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC CTTCTGAACC
   AAGATTTCTT TTAGTTTAAT CCTATTCTAA ACATAGACTA CTTATAAAAG GAAGACTTGG

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10/54

FIG. 7(CONTINUED 1).

+2 oGlyPheCys IleHisTyrAsn IleValMet ProGlnPhe ThrGluAlaVal SerProSe

721 AGGGTTCTGC ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG TGAGTCCTTC
TCCCAAGACG TAGGTGATGT TGTAACAGTA CGGTGTTAAG TGTCTTCGAC ACTCAGGAAG

+2 rValLeuPro ProSerAlaLeu ProLeuAsp LeuLeuAsn AsnAlaIleThr AlaPheSe

781 AGTGCTACCC CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA CTGCCTTTAG
TCACGATGGG GGAAGTCGAA ACGGTGACCT GGACGAATTA TTACGATATT GACGGAAATC

+2 rThrLeuGlu AspLeuIleArg TyrLeuGlu ProGluArg TrpGlnLeuAsp LeuGluAs

841 TACCTTGGAA GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG ACTTAGAAGA
ATGGAACCTT CTGGAATAAG CTATAGAACT TGGTCTCTCT ACCGTCAACC TGAATCTTCT

+2 pLeuTyrArg ProThrTrpGln LeuLeuGly LysAlaPhe ValPheGlyArg LysSerAr

901 TCTATATAGG CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTTGGAA GAAAATCCAG
AGATATATCC GGTGAACCG TTGAAGAACC GTCCGAAAA CAAAACCTT CTTTTAGGTC

+2 gValValAsp LeuAsnLeuLeu ThrGluGlu ValArgLeu TyrSerCysThr ProArgAs

961 AGTGGTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA CACCTCGTAA
TCACCACCTA GACTTGGAAG ATTGTCTCCT CCATTCTAAT ATGTCGACGT GTGGAGCATT

+2 nPheSerVal SerIleArgGlu GluLeuLys ArgThrAsp ThrIlePheTrp ProGlyCy

1021 CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT GGCCAGGTTG
GAAGAGTCAC AGGTATTCCC TTCTTGATTT CTCTTGCTA TGGTAAAAGA CCGGTCCAAC

+2 sLeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys LeuHisAsnCys AsnGluCy

1081 TCTCCTGGTT AAACGCTGTG GTGGGAAC TGCTGTGTGT CTCCACAATT GCAATGAATG
AGAGGACCAA TTTGCGACAC CACCCTTGAC ACGGACAACA GAGGTGTAA CGTTACTTAC

+2 sGlnCysVal ProSerLysVal ThrLysLys TyrHisGlu ValLeuGlnLeu ArgProLy

1141 TCAATGTGTC CCAAGCAAAG TTAATAAAAA ATACCACGAG GTCCTTCACT TGAGACCAAA
AGTTACACAG GGTTCGTTTC AATGATTTTT TATGGTGCTC CAGGAAGTCA ACTCTGGTTT

+2 sThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal AlaLeuGluHis HisGluGl

1201 GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC ACCATGAGGA
CTGGCCACAG TCCCCTAACG TGTTTAGTGA GTGGCTGCAC CGGGACCTCG TGGTACTCCT

+2 uCysAspCys ValCysArgGly SerThrGly Gly
----->

1261 GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCCG CATCACCACC AGCAGCTCTT
CACACTGACA CACACGTCTC CCTCGTGTCC TCCTATCGGC GTAGTGCTGG TCGTCGAGAA

1321 GCCCAGAGCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA ACGTATGCGT TATCTCCATC
CGGGTCTCGA CACGTCACGT CACCGACTAA GATAATCTCT TGCATACGCA ATAGAGGTAG

1381 CTTAATCTCA GTTGTTTGCT TCAAGGACCT TTCATCTTCA GGATTTACAG TGCATTCTGA
GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT CCTAAATGTC ACGTAAGACT

11/54

FIG. 7 (CONTINUED 2).

1441 AAGAGGAGAC ATCAAACAGA ATTAGGAGTT GTGCAACAGC TCTTTTGAGA GGAGGCCTAA
 TTCTCCTCTG TAGTTTGTCT TAATCCTCAA CACGTTGTCTG AGAAAACTCT CCTCCGATT

1501 AGGACAGGAG AAAAGGTCTT CAATCGTGGA AAGAAAATTA AATGTTGTAT TAAATAGATC
 TCCTGTCCTC TTTTCCAGAA GTTAGCACCT TTCTTTTAAT TTACAACATA ATTTATCTAG

1561 ACCAGCTAGT TTCAGAGTTA CCATGTACGT ATTCCACTAG CTGGGTTCTG TATTTTCAGTT
 TGGTCGATCA AAGTCTCAAT GGTACATGCA TAAGGTGATC GACCCAAGAC ATAAAGTCAA

1621 CTTTCGATAC GGCTTAGGGT AATGTCAGTA CAGGAAAAAA ACTGTGCAAG TGAGCACCTG
 GAAAGCTATG CCGAATCCCA TTACAGTCAT GTCCTTTTTT TGACACGTTT ACTCGTGGAC

1681 ATTCCGTTGC CTTGGCTTAA CTCTAAAGCT CCATGTCCTG GGCCTAAAAT CGTATAAAAT
 TAAGGCAACG GAACCGAATT GAGATTTCTGA GGTACAGGAC CCGGATTTTA GCATATTTTA

1741 CTGGATTTTT TTTTTTTTTT TTGCGCATAT TCACATATGT AAACCAGAAC ATTCTATGTA
 GACCTAAAAA AAAAAAAAAA AACGCGTATA AGTGTATACA TTTGGTCTTG TAAGATACAT

1801 CTACAAACCT GGTTTTTAAA AAGGAACTAT GTTGCTATGA ATTAACTTG TGTCTATGCTG
 GATGTTTGA CCAAAAATTT TTCCTTGATA CAACGATACT TAATTTGAAC ACAGTACGAC

1861 ATAGGACAGA CTGGATTTTT CATATTTCTT ATTAATAATTT CTGCCATTTA GAAGAAGAGA
 TATCCTGTCT GACCTAAAAA GTATAAAGAA TAATTTTAAA GACGGTAAAT CTTCTTCTCT

1921 ACTACATTCA TGGTTTGGAA GAGATAAACC TGAAAAGAAG AGTGGCCTTA TCTTCACTTT
 TGATGTAAGT ACCAAACCTT CTCTATTTGG ACTTTTCTTC TCACCGGAAT AGAAGTGAAA

1981 ATCGATAAGT CAGTTTATTT GTTTCATTGT GTACATTTTT ATATTCTCCT TTTGACATTA
 TAGCTATTCA GTCAAATAAA CAAAGTAACA CATGTAAAAA TATAAGAGGA AAAGTGAAT

2041 TAACTGTTGG CTTTTCTAAT CTTGTAAAT ATATCTATTT TTACCAAAGG TATTTAATAT
 ATTGACAACC GAAAAGATTA GAACAATTTA TATAGATAAA AATGGTTTCC ATAAATTATA

2101 TCTTTTTTAT GACAACTTAG ATCAACTATT TTTAGCTTGG TAAATTTTTT TAAACACAAT
 AGAAAAATA CTGTTGAATC TAGTTGATAA AAATCGAACC ATTTAAAAAG ATTTGTGTTA

2161 TGTATAGCC AGAGGAACAA AGATGATATA AAATATTGTT GCTCTGACAA AAATACATGT
 ACAATATCGG TCTCCTTGTT TCTACTATAT TTTATAACAA CGAGACTGTT TTTATGTACA

2221 ATTTCAATTCT CGTATGGTGC TAGAGTTAGA TTAATCTGCA TTTTAAAAAA CTGAATTGGA
 TAAAGTAAGA GCATACCACG ATCTCAATCT AATTAGACGT AAAATTTTTT GACTTAACCT

2281 ATAGAATTGG TAAGTTGCAA AGACTTTTTG AAAATAATTA AATTATCATA TCTTCCATTC
 TATCTTAACC ATTCAACGTT TCTGAAAAAC TTTTATTAAT TTAATAGTAT AGAAGGTAAG

2341 CTGTTATTGG AGATGAAAAT AAAAGCAAC TTATGAAAAGT AGACATTCAG ATCCAGCCAT
 GACAATAACC TCTACTTTTA TTTTTCGTTG AATACTTTCA TCTGTAAGTC TAGGTCGGTA

2401 TACTAACCTA TTCCTTTTTT GGGGAAATCT GAGCCTAGCT CAGAAAAACA TAAAGCACCT
 ATGATTGGAT AAGGAAAAAA CCCCTTTAGA CTCGGATCGA GTCTTTTTGT ATTTCTGTGA

2461 TGAAAAAGAC TTGGCAGCTT CCTGATAAAG CGTGCTGTGC TGTGCAGTAG GAACACATCC
 ACTTTTTCTG AACCGTCGAA GGAATTTTC GCACGACACG ACACGTCATC CTTGTGTAGG

2521 TATTTATTGT GATGTTGTGG TTTTATTATC TTAACTCTG TTCCATACAC TTGTATAAAT
 ATAAATAACA CTACAACACC AAAATAATAG AATTTGAGAC AAGGTATGTG AACATATTTA

12/54

FIG. 7(CONTINUED 3).

2581 ACATGGATAT TTTTATGTAC AGAAGTATGT CTCTTAACCA GTTCACTTAT TGTA CTCTGG
TGTACCTATA AAAATACATG TCTTCATACA GAGAATTGGT CAAGTGAATA ACATGAGACC

2641 CAATTTAAAA GAAATCAGT AAAATATTTT GCTTGTA AAA TGCTTAATAT CGTGCCTAGG
GTTAAATTTT CTTT TAGTCA TTTTATAAAA CGAACATTTT ACGAATTATA GCACGGATCC

2701 TTATGTGGTG ACTATTTGAA TCAAAAATGT ATTGAATCAT CAAATAAAAG AATGTGGCTA
AATACACCAC TGATAAACTT AGTTTTTACA TAACTTAGTA GTTTATTTTC TTACACCGAT

2761 TTTTGGGGAG AAAATT
AAAACCCCTC TTTTAA

FIG. 8. Additional oligonucleotides used for amplification of entire coding region

5'-1 TTTGTTTAAACCTTGGGAACTGG

5'-2 GTCCAGGTTTTGCTTTGATCC

13/54

FIG. 9. DNA Sequence Of Clones 4 & 7, Identical Clones Containing The Entire Open Reading Frame

```

1  TTTGTTTAAA CCTTGGGAAA CTGGTTCAGG TCCAGGTTTT GCTTTGATCC TTTTCAAAAA
   AAACAAATTT GGAACCCCTT GACCAAGTCC AGGTCCAAAA CGAAACTAGG AAAAGTTTTT

61  CTGGAGACAC AGAAGAGGGC TCTAGGAAAA AGTTTTGGAT GGGATTATGT GGAAACTACC
   GACCTCTGTG TCTTCTCCCG AGATCCTTTT TCAAAACCTA CCCTAATACA CCTTTGATGG

121 CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCCAC CCCAGTGCAG CCTTCCCCTG
   GACGCTAAGA GACGACGGTC TCGTCCGAGC CGCGAAGGTG GGGTCACGTC GGAAGGGGAC

181 GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCGCCGTG AGTGAGCTCT
   CGCCACCACT TTCTCTGAGC CCTCAGCGAC GAAGGTTTCA CGGGCGGCAC TCACTCGAGA

+2                               MetSer LeuPheGly LeuLeuLeu LeuThrSerAla LeuAlaGl
   ]-----

241 CACCCAGTC AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG CCCTGGCCGG
   GTGGGGTCAG TCGGTTTACT CGGAGAAGCC CGAAGAGGAC GACTGTAGAC GGGACCGGCC

+2 yGlnArgGln GlyThrGlnAla GluSerAsn LeuSerSer LysPheGlnPhe SerSerAs
   -----

301 CCAGAGACAG GGGACTCAGG CGGAATCCAA CCTGAGTAGT AAATTCCAGT TTTCCAGCAA
   GGTCTCTGTC CCCTGAGTCC GCCTTAGGTT GGACTCATCA TTTAAGGTCA AAAGGTCGTT

+2 nLysGluGln AsnGlyValGln AspProGln HisGluArg IleIleThrVal SerThrAs
   -----

361 CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG TGTCTACTAA
   GTTCCTTGTC TTGCCTCATG TTCTAGGAGT CGTACTCTCT TAATAATGAC ACAGATGATT

+2 nGlySerIle HisSerProArg PheProHis ThrTyrPro ArgAsnThrVal LeuValTr
   -----

421 TGGAAGTATT CACAGCCCAA GGTTTCCTCA TACTTATCCA AGAAATACGG TCTTGGTATG
   ACCTTCATAA GTGTCGGGTT CCAAAGGAGT ATGAATAGGT TCTTTATGCC AGAACCATAC

+2 pArgLeuVal AlaValGluGlu AsnValTrp IleGlnLeu ThrPheAspGlu ArgPheGl
   -----

481 GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACAACTT ACGTTTGATG AAAGATTTGG
   CTCTAATCAT CGTCATCTCC TTTTACATAC CTATGTTGAA TGCAAACCTAC TTTCTAAACC

+2 yLeuGluAsp ProGluAspAsp IleCysLys TyrAspPhe ValGluValGlu GluProSe
   -----

541 GCTTGAAGAC CCAGAAGATG ACATATGCAA GTATGATTTT GTAGAAGTTG AGGAACCCAG
   CGAACTTCTG GGTCTTCTAC TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC

+2 rAspGlyThr IleLeuGlyArg TrpCysGly SerGlyThr ValProGlyLys GlnIleSe
   -----

601 TGATGGAAC TATTAGGGC GCTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTT
   ACTACCTTGA TATAATCCCG CGACCACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG

+2 rLysGlyAsn GlnIleArgIle ArgPheVal SerAspGlu TyrPheProSer GluProGl
   -----

661 TAAAGGAAAT CAAATTAGGA TAAGATTTGT ATCTGATGAA TATTTTCCTT CTGAACCAGG
   ATTTCTTTTA GTTTAATCCT ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGGTCC

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FIG. 9 (CONTINUED). 14/54

+2 yPheCysIle HisTyrAsnIle ValMetPro GlnPheThr GluAlaValSer ProSerVa

721 GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTCACA GAAGCTGTGA GTCCTTCAGT
CAAGACGTAG GTGATGTTGT AACAGTACGG TGTAAAGTGT CTTGACACT CAGGAAGTCA

+2 lLeuProPro SerAlaLeuPro LeuAspLeu LeuAsnAsn AlaIleThrAla PheSerTh

781 GCTACCCCTC TCAGCTTTGC CACTGGACCT GCTTAATAAT GCTATAACTG CCTTTAGTAC
CGATGGGGGA AGTCGAAACG GTGACCTGGA CGAATTATTA CGATATTGAC GGAAATCATG

+2 rLeuGluAsp LeuIleArgTyr LeuGluPro GluArgTrp GlnLeuAspLeu GluAspLe

841 CTTGGAAGAC CTTATTTCGAT ATCTTGAACC AGAGAGATGG CAGTTGGACT TAGAAGATCT
GAACCTTCTG GAATAAGCTA TAGAACTTGG TCTCTCTACC GTCAACCTGA ATCTTCTAGA

+2 uTyrArgPro ThrTrpGlnLeu LeuGlyLys AlaPheVal PheGlyArgLys SerArgVa

901 ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTTGTT TTTGGAAGAA AATCCAGAGT
TATATCCGGT TGAACCGTTG AAGAACCGTT CCGAAAACAA AAACCTTCTT TTAGGTCTCA

+2 lValAspLeu AsnLeuLeuThr GluGluVal ArgLeuTyr SerCysThrPro ArgAsnPh

961 GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC CTCGTAACCT
CCACCTAGAC TTGGAAGATT GTCTCTCCA TTCTAATATG TCGACGTGTG GAGCATTGAA

+2 eSerValSer IleArgGluGlu LeuLysArg ThrAspThr IlePheTrpPro GlyCysLe

1021 CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC CAGGTTGTCT
GAGTCACAGG TATTCCTTC TTGATTTCTC TTGGCTATGG TAAAAGACCG GTCCAACAGA

+2 uLeuValLys ArgCysGlyGly AsnCysAla CysCysLeu HisAsnCysAsn GluCysGl

1081 CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA ATGAATGTCA
GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTAAACGT TACTTACAGT

+2 nCysValPro SerLysValThr LysLysTyr HisGluVal LeuGlnLeuArg ProLysTh

1141 ATGTGTCCCA AGCAAAGTTA CTAAAAATA CCACGAGGTC CTTAGTTGA GACCAAAGAC
TACACAGGGT TCGTTTCAAT GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG

+2 rGlyValArg GlyLeuHisLys SerLeuThr AspValAla LeuGluHisHis GluGluCy

1201 CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC ATGAGGAGTG
GCCACAGTCC CCTAACGTGT TTAGTGAGTG GCTGCACCGG GACCTCGTGG TACTCCTCAC

+2 sAspCysVal CysArgGlySer ThrGlyGly
----->

1261 TGACTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC AGCTCTTGCC
ACTGACACAC ACGTCTCCCT CGTGTCTCTC TATCGGCGTA GTGGTGGTCG TCGAGAACGG

1321 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT CTCCATCCTT
GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA GAGGTAGGAA

1381 AATCTCAGTT GTTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG
TTAGAGTCAA CAAACGAAGT TCCTGGAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC

1441 AGGAGACATC AAACAGAATT AGGAGTTGTG CAA
TCCTCTGTAG TTTGTCTTAA TCCTCAACAC GTT

15/54

FIG. 10. Predicted Full-length Polypeptide Sequence

1 MSLFGLLLLT SALAGQRQGT QAESNLSSKF QFSSNKEQYG VQDPQHERII
51 TVSTNGSIHS PRFPHTYPRN TVLVWRLVAV EENVWIQLTF DERFGLEDPE
101 DDICKYDFVE VEEPSDGTIL GRWCGSGTVP GKQISKGNQI RIRFVSDEYF
151 PSEPGFCIHY NIVMPQFTEA VSPSVLPESA LPLDLLNNAI TAFSTLEDLI
201 RYLEPERWQL DLEDLYRPTW QLLGKAFVFG RKSrvVDLNL LTEEVRLYSC
251 TPRNFSVSIR EELKRTDTIF WPGCLLVXRC GGNCACCLHN CNECQCVP SK
301 VTKKYHEVLQ LRPKTGVRGL HKSLTDVALE HHEECDCVCR GSTGG

16/54

FIG. 11.

Alignment of VEGF-X with Other VEGFs

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      *           20           *           40           *
VEGF_HUMAN : ----- : -
PLGF_HUMAN : ----- : -
VEGB_HUMAN : ----- : -
VEGC_HUMAN : ----- : -
VEGD_HUMAN : ----- : -
990126vegx : MSLFGLLLLT SALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII : 50

      60           *           80           *           100
VEGF_HUMAN : ----- : -
PLGF_HUMAN : ----- : -
VEGB_HUMAN : ----- : -
VEGC_HUMAN : ----- : -
VEGD_HUMAN : ----- : -
990126vegx : TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWVQLTFDERFGLEDPE : 100

      *           120           *           140           *
VEGF_HUMAN : ----- : -
PLGF_HUMAN : ----- : -
VEGB_HUMAN : ----- : -
VEGC_HUMAN : -----MHLLGFFSVACSLLAALLPGPREAPAAAA : 30
VEGD_HUMAN : -----MYREWVVVNV : 10
990126vegx : DDICKYDFVEV--EEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE : 148

      160           *           180           *           200
VEGF_HUMAN : -----MN : 2
PLGF_HUMAN : -----MP : 2
VEGB_HUMAN : ----- : -
VEGC_HUMAN : AFESGLDLSDAEPDAGEATAYASKDLEEQLRVSSVDELMTVLYPEYWKM : 80
VEGD_HUMAN : FMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE : 60
990126vegx : YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLED : 198

      *           220           *           240           *
VEGF_HUMAN : FLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHHEVVKFMD-VYQRSY : 51
PLGF_HUMAN : VMRLFPCFLQLLAGLALPAVPPQQWALSAGNGSSEVEVVPFQE-VWGRSY : 51
VEGB_HUMAN : ---MSPLLRRLLLAALLQLAPAPVSQPDAPGHQRKVVSVID-VYTRAT : 46
VEGC_HUMAN : YKCLRKGWQHNRQANLNSRTEETIKFAAAHYNTEILKSIDNEWKRKTQ : 130
VEGD_HUMAN : DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWQRTQ : 110
990126vegx : LIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKSRVVDLNLLEEVRLY : 248

      260           *           280           *           300
VEGF_HUMAN : CHPIETLVDFQEPYDEIEYIFKPSCVPLMRCGG---CCND--EGLECVP : 96
PLGF_HUMAN : CRALERLVDVVSSEYPSEVEHMFSPSCVSLLRCTG---CCGD--ENLHCVP : 96
VEGB_HUMAN : CQPREVVVPLTVELMGTVAKQLVPSCVTVQRCGG---CCPD--DGLCVP : 91
VEGC_HUMAN : CMPREVCIDVGKBFQVATNTFFKPPCVSVYRCGG---CCNS--EGLQCMN : 175
VEGD_HUMAN : CSPRETCVEVASLGLKSTNTFFKPPCVNVFRCGG---CCNE--ESLICMN : 155
990126vegx : SCTPRNFSVSIREELKRTDTIFWEGCLLVKRCGGNCACCLHNCNECQCV : 298

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17/54

FIG. 11 (CONTINUED).

	*	320	*	340	*	
VEGF_HUMAN	:	TEESNITMQIMRTKPHQG-----	QHIGEMSFLQHNKCECRPKKDRARQEK	:	141	
PLGF_HUMAN	:	VETANVTMQLLKIRSGDR-----	PSYVELTFSQHVRCCECRPLREKMKPER	:	141	
VEGB_HUMAN	:	TGQHQVRMQILMIRYPS-----	SQLGEMSLEEHSQCECRPKKKDSAVKP	:	135	
VEGC_HUMAN	:	TSTSLSKTLFEITVPLSQG---	PKPVTISFANHTSCRCMSKLDVYRQVH	:	222	
VEGD_HUMAN	:	TSTSYISKQLFEISVPLTSV---	PELVPVKVANHTGCKCLPTAPRHPYSI	:	202	
990126vegx	:	SKVTKKYHEVLQLRPKTGVRGLHKS LTDVALEHH EECDCVCRGSTG---		:	345	

	360	*	380	*	400	
VEGF_HUMAN	:	KSVRGKGKGQKRKRKKSRYKSWSP-----		:	166	
PLGF_HUMAN	:	-----		:	-	
VEGB_HUMAN	:	DSPR-----		:	139	
VEGC_HUMAN	:	SIIRSLPATLPQCQAANKTCPTNYMWNHICRCLAQEDFMFSSDAGDDS		:	272	
VEGD_HUMAN	:	IRRSIQIPEEDRCSHKKLCPIDMLWDSNKCKCVLQEENPLAGT-----		:	246	
990126vegx	:	-----		:	-	

	*	420	*	440	*	
VEGF_HUMAN	:	-----		:	-	
PLGF_HUMAN	:	-----		:	-	
VEGB_HUMAN	:	-----		:	-	
VEGC_HUMAN	:	TDGFHDICGPNKELDEETCQCVCVRAGLRPASCGPHKELDRNSCQCVCVKNK		:	322	
VEGD_HUMAN	:	-----		EDHSHLQEPALCGP	:	260
990126vegx	:	-----			:	-

	460	*	480	*	500	
VEGF_HUMAN	:	-----	CGPCSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNER	:	206	
PLGF_HUMAN	:	-----	CGDAVPRR-----	:	149	
VEGB_HUMAN	:	-----	PLCPRCTQHHQRPDPRTCRCRCRRRSFLRCQGRGLELNP	:	179	
VEGC_HUMAN	:	LFPSQCGANREFDENTCQCVCVKRTCPRNQPLNPGKCAECTESPQKCLLK		:	372	
VEGD_HUMAN	:	HMMFEDDRCEVCVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLFPD		:	310	
990126vegx	:	-----		:	-	

	*	520	*	540	*	
VEGF_HUMAN	:	TCRCDKPRR-----		:	215	
PLGF_HUMAN	:	-----		:	-	
VEGB_HUMAN	:	TCRCRKLRR-----		:	188	
VEGC_HUMAN	:	GKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRVCPSYWKRQMS---		:	419	
VEGD_HUMAN	:	TCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP-----		:	354	
990126vegx	:	-----		:	-	

18/54

FIG. 12.

Variant Polypeptide Sequences

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      *           20           *           40           *
FL_seq : MSLFGLLLLSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII : 50
clone41 : MSLFGLLLLSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII : 50
clone20 : MSLFGLLLLSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII : 50

      60           *           80           *           100
FL_seq : TVSTNGSIHSPRFPHPTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE : 100
clone41 : TVSTNGSIHSPRFPHPTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE : 100
clone20 : TVSTNGSIHSPRFPHPTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE : 100

      *           120           *           140           *
FL_seq : DDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYF : 150
clone41 : DDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYF : 150
clone20 : DDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYF : 150

      160           *           180           *           200
FL_seq : PSEFGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLI : 200
clone41 : PSEPSNRGGKIIQLHTS----- : 167
clone20 : PSEFGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLI : 200

      *           220           *           240           *
FL_seq : RYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLEEVRLYSC : 250
clone41 : ----- : -
clone20 : RYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLE----- : 243

      260           *           280           *           300
FL_seq : TPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK : 300
clone41 : ----- : -
clone20 : ----- : -

      *           320           *           340
FL_seq : VTKKYHEVLQLRPKTGVRGLHKS LTDVALEHHEECDVCVRGSTGG : 345
clone41 : ----- : -
clone20 : -----EVLQLRPKTGVRGLHKS LTDVALEHHEECDVCVRGSTGG : 282

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19/54

FIG. 13. Primers for Expression of VEGF-X*E.coli expression of domain-*

vegX-6	AATTGGATCCGAGAGTGGTGGATCTGAACC
vegX-7	AATTGGATCCGGGAAGAAAATCCAGAGTGG
vegX-8	GGTTGAATTCATTATTTTTTAGTAACTTTGCTTGGGACAC
vegX-9	AATTGAATTCATTATCCTCCTGTGCTCCCTC

Baculovirus/insect cell expression of full-length protein-

vegbac1	AATTGGATCCGGAGTCTCACCATCACCACCATCATGAATCCAACCTGAGTAGTAAATTC
	C
vegbac2	AATTGAATTCGCTATCCTCCTGTGCTCCCTCTGC

20/54

FIG. 14.

>3993180H1 LUNGNON03 INCYTE
CACAAATCACTCACCACGCTGGCCCTGGAGCACCATGAGGNGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCC
GCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCAT
CCTTAATCTCAGTTGTTTGTCTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAG
AATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCTAAAGGACAGGAGAAANAGGTCTT

>3510192H1 CONCN01 INCYTE
TGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTCTCAAGGACCTT
TCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAAATTAGGAGTTGTGCAACAGCTCTTTTGAGAG
GAGGCCATAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTT
TCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTT

>2559870H1 ADRETUT01 INCYTE
CACGAGTGCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCA
TGAGGAGTTGTGACTGTGTGTGCAGAGGGAGCACAGGGGATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGC
AGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTCTCAAGGACCTTTCA
TCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGA

>3979767H1 LUNGTUT08 INCYTE
GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGC
GTTATCTCCATCCTTAATCTCAGTTGTTTGTCTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAG
ACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCATAAGGACAGGAGAAAAGGTCTTCAATCGTG
GAAAGAAATTAATGTTGTATTAAATAGACACCAGCT

>3980011H1 LUNGTUT08 INCYTE
GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGC
GTTATCTCCATCCTTAATCTCAGTTGTTTGTCTCAAGGACCTTTTCATCTTCAGGATTTACATGCATTCTGAAAGAGGAGA
CATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCATAAGGACAGGAGAAAAGGTCTTCAATCGTG
AAAGAAAATTAATGTTGTATTAAATAGATCACCA

>4825396H1 BLADDIT01 INCYTE
GAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACGTGTGCCTGTTGTCTCCACAAT
GCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCTTCAGTTGAGACCAAAGACCGGTGTG
AGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAG
AGGATAGCCGCATCACCACCA

>3073703H1 BONEUNT01 INCYTE
AGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGT
GTCCATAAGGGAAGAATAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACCT
GTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCTTTCAG
TTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCA

>1302516H1 PLACNOT02 INCYTE
AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCTTCTAACAGAGGAGGTAAGATTATAC
AGCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAATAAGAGAACCGATACCATTCTTCTGGCCAGGTTGTCT
CCTGGTTAAACGCTGTGGTGGGAACCTGTGCCTGTTGTCTCCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTT
ACTAAAAAATACCACGAGGTCC

>3684109H1 HEANOT01 INCYTE
ATTTTCATCTTCAGGATTTACAGTGCATTCTGAAANAGGAGAAATCAAAACANAATTAGGAGTTGTGCAACAGCTCTTTTGA
GAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAANAAAATTAAATGTTGTATTAAATAGATCACCAGCTA
GTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGTTCTGTATTTTCAGTTCTTTTGATACGGCTTAGGGTAATGTCA
TACAGGAAAAAACTGTGCAAGTGAGCAGCTGATTCCGTTGCCTTGCTT

>4713188H1 BRAIHCT01 INCYTE
CAAAGTTACTAAAAAATACCACGAGGTCTTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCG
ACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAG
CTCTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTTGT
TTGCT

>458823H1 KERANOT01 INCYTE
ANGAGTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTT
GTTTGNITCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTG
CAACAGCTCTTTTGAGAGGAGGCCATAAGGNCAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAA
ATAGATC

>1303909H1 PLACNOT02 INCYTE
AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCTTCTAACAGAGGAGGTAAGATTATAC
AGCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAATAAGAGAACCGATACCATTCTTCTGGCCAGGTTGTCT
CCTGGTTAAACGCTGTGGTGGGAACCTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAG

21/54

FIG. 14 (CONTINUED).

>2739211H1 OVARNOT09 INCYTE
 GTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGA
 GAAAAGGTCTTCAATCGTGGAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACG
 TATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAA
 GTGAGCACCTGAT

>3325591H1 PTHYN03 INCYTE
 TGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGAAAATTAAATGTTGTATT
 AAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGTTCTGTATTTTCAGTTCTTTTCGATACG
 GCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACCTAAAGCNCC
 ATGTCNNGGGCNAANCGAAAAAT

>3733565H1 SMCCN01 INCYTE
 CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGNAAGANGAGACATCAAACAG
 AATTAGGNGTTGTGCAAAAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTNCAATCGTGGAAGNAAATT
 AAATGTTGTATNAAATNGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGNCNGTATTCAGTCT
 TTCGGAACGGCTTAGGGTAATGTCAGTACAGGANAAAACTGTGCAGTGAG

>3554223H1 SYNON01 INCYTE
 ATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGTTCTGTATTTTCAGTTCTTTTCGAT
 ACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACCTCTAAAG
 CTCCATGTCCTGGGCCTAAATCGTATAAAATCTGGATTTTNTTTTTTTTTTGCGCATATTCACATATGTAAACCAGN
 ACATTCTATGTACNACAAACCTGGTTTTTAAAAAGGAAC

>4507477H1 OVARTD01 INCYTE
 GGCTAGTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAAT
 GTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACCTCTAAAGCTCCATGTCCTGGGCC
 TAAAATCGTATAAAATCTGGA

>4163378H1 BRSTN032 INCYTE
 AATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGNTCTGTATTTTCAGTTCTTTTCGATACG
 GCTTAGGGTAATGTCAGTACAGGAAAAAGCTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACCTCTAAAGCTCC
 ATGTCCTGGGCCTAAAAATCGTATA

>2054675H1 BEPINOT01 INCYTE
AAAGGAACATATGTTGCTATGAATTAACCTTGTGTCGTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATAATT
TCTGCCATTTAGAGAAGAGAACTACATTTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTT
TATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAA
TCTTGTTAAATATATCTATTTTTACCAAAGGTATTTAATATTCTTTTTTA
>3993180H1 LUNGNON03 INCYTE
CACAAATCACTACCAGCTGGCCCTGGAGCACCATTGAGGNGTGTGACTGTGTGTGTCAGAGGGAGCACAGGAGGATAGCC
GCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCAT
CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAACAG
AATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCTAAAGGACAGGAGAAAGGTCTT
>3510192H1 CONCNOT01 INCYTE
TGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTT
TCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCAACAGCTCTTTTGAGAG
GAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTT
TCAGAGTTACCATGTACGTATTCCTAGCTGGGTTCTGTATTT
>4164633H1 BRSTNOT32 INCYTE
CTTGTTAAATATATCTATTTTTACCAAAGGTATTTAATATTCTTTANTTATGACAACTTAGATCAACTATTTTTAGCTTG
GTAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATG
TATTTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAAGTGAATTGGAATAGAATTGGTAAGTTGCA
AAGACTTTTTGANAATAATTAATTTATCATATCTTCCATTCTGTTATTGGGGGAGAAAAT
>2559870H1 ADRETUT01 INCYTE
CACGAGGTCTTTCAGTTGAGACCAAAGACCGGTGTGTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGACCA
TGAGGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGGGGGATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGC
AGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTCA
TCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGA
>3817470H1 BONSTUT01 INCYTE
TTAAAAAGGAACATGTTGCTATGAATTAACCTTGTGTGTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAA
AATTTCTGCCATTTAGAGAAGAGAACTACATTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTC
ACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTC
TAATCTGTTAAATATATCTATTTTTACCAAAGGTATTTAATATTCTTT
>3979767H1 LUNGTUT08 INCYTE
GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGC
GTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAG
ACATCAAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTG
GAAAGAAATTAATGTTGTATTAAATAGACACCAGCT
>3980011H1 LUNGTUT08 INCYTE
GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGC
GTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACATGCATTCTGAAAGAGGAGA
CATCAAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGG
AAAGAAAATTAATGTTGTATTAAATAGATCACCA
>4825396H1 BLADDIT01 INCYTE
GAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACGTGCGCTGTTGTCTCCACAATT
GCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCTTCAGTTGAGACCAAGACCGGTGTG
AGGGGATTGCACAAATCACTCACCAGCTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGG
AGGATAGCCGCATCACCACCA
>3073703H1 BONEUNT01 INCYTE
AGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGT
GTCCATAAGGGAAGAACAAGAGAACCGATACCAATTTCTGGCCAGGTGTCTCCTCGTTAAACGCTGTGGTGGGAACCT
GTGCGCTTGTGCTCCACAATTGCAATGCAATGTGTGCCAAGCAAAGTTACTAAAAAATACCACGAGGTCTTCAG
TTGAGACCAAGACCGGTGTGTCAGGGGATTGCACAAATCA
>862169H1 BRAITUT03 INCYTE
AGATGATATAAAATATTGTGCTCTGACAAAAATACATGTATTTTCATTCTCGTATGGTGTGAGATTAGATTAAATCTGCA
TTTTAAAAAAGTGAATTGGAATAGAATTGCTAAGTTGCAAGACTTTTGAATAAATTAATTTATCATATCTTCCATTC
CTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCTATTCTTTTTT
CGGCAATCTCAGCCTAGC
>4201385H1 BRAITUT29 INCYTE
TTTTTAAAAAGGAACATTTGTGCTATGAATTAACCTTGTGTGCTGCTGATAGCACAGACTGGATTTTTCATATTTCTTAT
TAAATTTCTGCCATTTAGAGAAGAGAACTACATTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAGAGTGGCCTATCT
TCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTATATTCTCCTTTGACATATAACTGTTGGCTTTT

FIG. 15 (CONTINUED 1). 23/54

CTAATCTGTTAAATATATCTATTTTTTACCAAAGGTATTTAATAT
 >1302516H1 PLACNOT02 INCYTE
 AGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTTCTTCTGAACCTTCTAACAGAGGAGGTAAGATTATAC
 AGCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCAGATACCATTTTCTGGCCAGGTTGTCT
 CCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTT
 ACTAAAAAATACCACGAGGTCC
 >3684109H1 HEANOT01 INCYTE
 ATTTTCATCTTCAGGATTTACAGTGCATTCTGAAANAGGAGAAATCAAACANAATTAGGAGTTGTGCAACAGCTCTTTTGA
 GAGGAGGCCTAAAGGACAGGAGAAAAAGGTCTTCAATCGTGGAAANAAAAATTAATGTTGTATTAAATAGATCACCAGCTA
 GTTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAG
 TACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTT
 >2549720H1 LUNGTUT06 INCYTE
 TTAGCTTGGNAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAA
 AATACATGTATTTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGT
 AAGTTGCAAAGACTTTTTGAAAAATAATTAAATTATCATATCTTCCATTCTGTTATTGGAGATGAAAAATAAAAGCAACT
 TATGANAGTAG
 >877279H1 LUNGAST01 INCYTE
 CTTTTTTATGACAACTTAGATCAACTATTTTTTAGCTTGGTAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAACAAA
 GATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCAT
 TTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGGCTTTTTGAAAAATAATTAAATTATCATATCTTCCATTCC
 TGTATTGNGG
 >4713188H1 BRAIHCT01 INCYTE
 CAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCG
 ACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAG
 CTCTTGCCAGAGCTGTGCAGTGCAGTGCCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGT
 TTGCT
 >2171082H1 ENDCNOT03 INCYTE
 AGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTA
 TATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTTACCAAAGGTATTTAATATT
 CTTTTTTATGACAACTTAGATCAACTATTTTTTAGCTTGGTAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAACAAA
 GATGA
 >875860H1 LUNGAST01 INCYTE
 CTGGATTTTTCATATTTCTTATTAAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAAGAGATAAAC
 TGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTATATTCTCCT
 TTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTTACCAAAGGTATTTAATATTCTTTTTTAT
 GAC
 >706168H1 SYNORAT04 INCYTE
 GCTCATATTCACATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGANCTATGTTGCTATGAAT
 TAAACTTGTGTGCTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAAATTTCTGCCATTTAGAAGAAGAGAAC
 TACATTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCANTTTATCGATAAGTCAGTTTATTTGT
 TTCA
 >458823H1 KERANOT01 INCYTE
 ANGAGTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCASTT
 GTTTGNNTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAAGAGGAGACATCAAAACAGAATTAGGAGTTGTG
 CAACAGCTCTTTTGAGAGGAGGCCTAAAGGNCAGGAGAAAAAGGTCTTCAATCGTGGAAAGAAAATTAATGTTGTATTAA
 ATAGATC
 >538436H1 LNODNOT02 INCYTE
 AAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTG
 CATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTTATCATATCTTCCAT
 TCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTCCAGATCCAGCCATTACTAACCTAT
 >1303909H1 PLACNOT02 INCYTE
 AGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTTCTTCTGAACCTTCTAACAGAGGAGGTAAGATTATAC
 AGCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCAGATACCATTTTCTGGCCAGGTTGTCT
 CCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAG
 >2739211H1 OVARNOT09 INCYTE
 GTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGA
 GAAAAGGTCTTCAATCGTGGAAAGAAAATTAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACG
 TATTTCCACTAGCTGGTCTGTATTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCA
 GTGAGCACCTGAT

>2550343H1 LUNGUT06 INCYTE
FGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCNAACTCTTGTTAAATATATCTATTTTTACCAAAG
GTATTTAATATTCTTTTTTATGACAACCTTAGATCAACTATTTTTAGCTTGGTAAATTTTTCTAAACACAATTGTTATAGC
CAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTTCATTCTCGTATGGTGCTA
>5321148H1 FIBPFEN06 INCYTE
CACAAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGNCAAAAATACATGTATTTTCATTCTCGTA
TGTTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAA
TAATTAAATTATCATATCTTCCATTCTGTTATTGGAGATGAAAAATAAAAAGCAACTTATGAAAGTAAATTTCAGATCCAC
CATTACTAAC
>879495H1 THYRNOT02 INCYTE
ATTTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAA
AGACTTTTTGAAAAATAATTAAATTATCATATCTTCCATTCTGTTATTGGAGATGAAAAATAAAAAGCAACTTATGAAAGT
AGACATTTCAGATCCAGCCATTACTAACCTATTCTTTTTTTGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCT
TGAAAAA
>3325591H1 PTHYNOT03 INCYTE
TGCAACAGCTCTTTTGAGAGGAGCCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAATGTTGTATT
AAATAGATCACCAGCTAGTTTCAGAGTTTACCATGTACGTATTCCACTAGCTGGGTCTGTATTTCAGTTCTTTTCGATACG
GCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCCTTGCTTAACCTTAAAGCNC
ATGTCNNGGGCNAAAANCGAAAAAT
>543890H1 OVARNOT02 INCYTE
TTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGNATAGAATTGGTAAGTTGCAAAGNCTT
TTTGAAAAATAATTAAATTATCATATCTTCCATTCTGTTATTGGAGGATGAAAAATAAAAAGCAACTTATGAAAGTAGG
ACATTTCAGATC
>3733565H1 SMCCNOS01 INCYTE
CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGNAAGANGAGACATCAAACAG
AATTAGNGTTGTGCAAAAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTNCAATCGTGGAAAGNAAATT
AAATGTTGTATNAAATNGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNCNGTATTTCAGTCT
TTCGGAACGGCTTAGGGTAATGTCAGTACAGGANAAAACTGTGCAGTGAG
>4641939H1 PROSTMT03 INCYTE
GTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAATTAACTTGTGTCCATGCTGATAGGACAGACTGGAT
TTTNCATATTTCTTATTAAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGNAGAGATAAACCTGAAA
GAAAGATGGCCTTATCTTCACCTTATCGATAAGTCAGTTTATTGTTTCATGTGTACATTTTATATCTCTCTTTGACAT
ATAACGTGGCTTT
>2007780H1 TESTNOT03 INCYTE
TTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTACCAAAGGTATTTAAT
ATTCTTTTTTATGACAACCTTAGATCAACTATTTTTAGCTTGGTAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAAC
AAAGATGATATAAAATATTGTTGCTCTGANAAAAATACATGTA
>3085331H1 HEANOT03 INCYTE
GCTCATATTCACATATGTAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATTGCTATGAATT
AACTTGTGTCTGTGCTGATAGGACAGACTGGNTTTTTCATATTTCTTATTANAATTTCTGCCATTAGAAGAAGAGAACTA
CATTTCATGGTTTTGGAAGAGATAAACCTGAAAAGAAGAGTGCCCTATTTACCTTTATCGATAAGTCAGT
>3414043H1 PTHYNOT04 INCYTE
GCTCATATTCACATATGTAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATTGCTATGAAT
TAACTTGTGTCTGTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAAATTTCTGCCATTTAGAAGAAGAGAACT
TACATTCATGGTTTTGGAAGAGATAAACCTGAAA
>3705963H1 PENCNOT07 INCYTE
ANACTGTGCAAGTGAGCACCTGATTCGGTTGCTTAACCTCTAAAGCTCCATGTCTGGGCCCTAAAATCGTATAAAA
TCTGGAGTTTTTTTTTTTTTTTTTTTTGCTCATATTCACATATGTAACCAGAACATTCTATGTACTACAAACCTGGTTTTTA
AAAAGGAACATATGTTGCTATGAATTAACTTGTGTCTGTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAAAT
TTCTGCCATTAGAAGAAGAGAACTACNTTCANGGTTTGGAAGAGATAACCCTGAAAAGANGGG
>5137051H1 OVARDIT04 INCYTE
AAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTNNTTGAAAAATAATTAAATTATCATATCTTCCATTCTCTGT
TATTGAGATGAANATAAAAAGCAACTTATGAAAGTAGACATTTCAGATCCAGCCATTACTAACCTATTCTTTTTTGGGG
AAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAAGACTTGGCAGCTTCTGTATAAAGCGTGCTGTNTGTCA
GTAGGAACACATCTTATTTATTGTGATGNTGTGGTTTATTAT
>3554223H1 SYNONOT01 INCYTE
ATTAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTTCGAT
ACCGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCCTTGCTTAACTCTAAAG

[illegible]

26/54

FIG. 16.

VEGFE1	AAAATGTATGGATACAACTTAC	22
VEGFE2	GTTTGATGAAAGATTGGGCTTG	23
VEGFE3	TTTCTAAAGGAAATCAAATTAG	22
VEGFE4	GATAAGATTTGTATCTGATG	20
VEGFE5	GATGTCTCCTCTTTCAG	17
VEGFE6	GCACAACTCCTAATTCTG	18
VEGFE7	AGCACCTGATTCCGTTGC	19
VEGFE8	TAGTACATAGAATGTTCTGG	20
VEGFE9	AAGAGACATACTTCTGTAC	19
VEGFE10	CCAGGTACAATAAGTGAAGTGA	21

27/54

FIG. 17.

+3 M N I F L L
N L L T E E V R L Y
]-----

1 AGGAAATCAA ATTAGGATAA GATTGTATC TGATGAATAT TTCCTTCTG
AACCTTCTAA CAGAGGAGGT AAGATTATAC
TCCTTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAAGAC
TTGGAAGATT GTCTCCTCCA TTCTAATATG

+3 S C T P R N F S V S I R E E L K R
T D T I F W P G C L
-----]

81 AGCTGCACAC CTCGTAACCT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG
AACCGATACC ATTTTCTGGC CAGGTTGTCT
TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCTTC TTGATTTCTC
TTGGCTATGG TAAAAGACCG GTCCAACAGA
-2 <-----

+3 L V K R C G G N C A C C L H N C N
E C Q C V P S K V

161 CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA
ATGAATGTCA ATGTGTCCCA AGCAAAGTTA
GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT
TACTTACAGT TACACAGGGT TCGTTTCAAT
-2 -----

+3 T K K Y H E V L Q L R P K T G V R
G L H K S L T D V A

+1 V S G
D C T N H S P T W P
]-----

241 CTAAAAAATA CCACGAGGTC CTTCAGTTGA GACCAAAGAC CGGTGTCAGG
GGATTGCACA AATCACTCAC CGACGTGGCC
GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG GCCACAGTCC
CCTAACGTGT TTAGTGAGTG GCTGCACCGG
-2 -----

-----[
+3 L E H H E E C D C V C R G S T G G

28/54

FIG. 17 (CONTINUED).

```

>
      +2                V   Q   R   E   H   R   R
I   A   A   S   P   P   A   A   L   A
      ]-----
-----
      +1   W   S   T   M   R   S   V   T   V   C   A   E   G   A   Q   E   D
S   R   I   T   T   S   S   S   C
-----
-----
321   CTGGAGCACC ATGAGGAGTG TGA CTGTGTG TGCAGAGGGA GCACAGGAGG
      ATAGCCGCAT CACCACCAGC AGCTCTTGCC
          GACCTCGTGG TACTCCTCAC ACTGACACAC ACGTCTCCCT CGTGTCTCTCC
      TATCGGCGTA GTGGTGGTCG TCGAGAACGG
-----
      +2   Q   S   C   A   V   Q   W   L   I   L   L   E   N   V   C   V   I
S   I   L   N   L   S   C   L   L   Q
-----
-----
      +1   P   E   L   C   S   A   V   A   D   S   I   R   E   R   M   R   Y
L   H   P
-----
----->
401   CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT
      CTCCATCCTT AATCTCAGTT GTTTGCTTCA
          GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA
      GAGGTAGGAA TTAGAGTCAA CAAACGAAGT
-----
      +2   G   P   F   I   F   R   I   Y   S   A   F
----->
481   AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG AGGAGACATC
      AAACAGAATT AGGAGTTGTG CAACAGCTCT
          TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC TCCTCTGTAG
      TTTGTCTTAA TCCTCAACAC GTTGTGCGAGA
-----
561   TTTGAGAGGA GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAAG
      AAAATTAAAT GTTGATTATA ATAGATCACC
          AAACCTCTCT CCGGATTTC TGTCTCTCTT TCCAGAAGTT AGCACCTTTC
      TTTTAATTTA CAACATAATT TATCTAGTGG
-----
641   AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTTCGTGAT
      TTCAGTTCTT TCGATACGGC TTAGGGTAAT
          TCGATCAAAG TCTCAATGGT ACATGCATAA GGTGATCGAC CCAAGACATA
      AAGTCAAGAA AGCTATGCCG AATCCCATTA
-----
721   GTCAGTACAG GAAAAAACT GTGCAAGTGA GCACCTGATT CCGTTGCCTT
      GGCTTAACTC TAAAGCTCCA TGTCTTGGGC
          CAGTCATGTC CTTTTTTTGA CACGTTCACT CGTGGACTAA GGCAACGGAA
      CCGAATTGAG ATTTGAGGT ACAGGACCCC
-----
801   CTAAAATCGT ATAAAATCTG GA
      GATTTTAGCA TATTTTAGAC CT

```

29/54

FIG. 18.

```

      +3                               M N I F L L
N L L T E E V R L Y                ]-----
-----
      1 AGGAAATCAA ATTAGGATAA GATTTGTATC TGATGAATAT TTTCCTTCTG
AACCTTCTAA CAGAGGAGGT AAGATTATAC
      TCCTTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAAGAC
TTGGAAGATT GTCTCCTCCA TTCTAATATG

      +3 S C T P R N F S V S I R E E L K R
T D T I F W P G C L
      -----]-----
-----
      81 AGCTGCACAC CTCGTAAGTT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG
AACCGATACC ATTTTCTGGC CAGGTTGTCT
      TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCTTTC TTGATTTCTC
TTGGCTATGG TAAAAGACCG GTCCAACAGA
      -2 <-----
-----
      +3 L V K R C G G N C A C C L H N C N
E C Q C V P S K V
      -----
-----
      161 CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA
ATGAATGTCA ATGTGTCCCA AGCAAAGTTA
      GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT
TACTTACAGT TACACAGGGT TCGTTTCAAT
      -2 -----
-----
      +3 T K K Y H E V L Q L R P K T G V R
G L H K S L T D V A
      -----
-----
      +1                               V S G
D C T N H S P T W P                ]-----
-----
      241 CTAAAAAATA CCACGAGGTC CTTCAAGTGA GACCAAAGAC CGGTGTCAGG
GGATTGCACA AATCACTCAC CGACGTGGCC
      GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG GCCACAGTCC
CCTAACGTGT TTAGTGAGTG GCTGCACCGG

```

30/54
FIG. 18 (CONTINUED 1).

```

-2 -----
-----[
+3 L E H H E E C D C V C R G S T G G
-----
>
+2 V Q R E H R R
I A A S P P A A L A
-----
]-----
+1 W S T M R S V T V C A E G A Q E D
S R I T T S S S C
-----
-----
321 CTGGAGCACC ATGAGGAGTG TGA CTGTGTG TGCAGAGGGA GCACAGGAGG
ATAGCCGCAT CACCACCAGC AGCTCTTGCC
GACCTCGTGG TACTCCTCAC ACTGACACAC ACGTCTCCCT CGTGTCTCTCC
TATCGGCGTA GTGGTGGTCG TCGAGAACGG
-----
+2 Q S C A V Q W L I L L E N V C V I
S I L N L S C L L Q
-----
-----
+1 P E L C S A V A D S I R E R M R Y
L H P
-----
----->
401 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT
CTCCATCCTT AATCTCAGTT GTTTGCTTCA
GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA
GAGGTAGGAA TTAGAGTCAA CAAACGAAGT
-----
+2 G P F I F R I Y S A F
----->
481 AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG AGGAGACATC
AAACAGAATT AGGAGTTGTG CAACAGCTCT
TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC TCCTCTGTAG
TTTGTCTTAA TCCTCAACAC GTTGTGCGAGA
-----
561 TTTGAGAGGA GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAG
AAAATTAAAT GTTGATTAA ATAGATCACC
AAACTCTCCT CCGGATTTC TGTCCTCTTT TCCAGAAGTT AGCACCTTTC
TTTAAATTAA CAACATAATT TATCTAGTGG
-----
641 AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTTCGTAT
TTCAGTTCTT TCGATACGGC TTAGGGTAAT
TCGATCAAAG TCTCAATGGT ACATGCATAA GTTGATCGAC CCAAGACATA
AAGTCAAGAA AGCTATGCCG AATCCCATTA
-----
721 GTCAGTACAG GAAAAAACT GTGCAAGTGA GCACCTGATT CCGTTGCCTT
GGCTTAACTC TAAAGCTCCA TGTCTGGGC

```

31/54

FIG. 18 (CONTINUED 2).

CAGTCATGTC CTTTTTTTGA CACGTTCACT CGTGGACTAA GGCAACGGAA
CCGAATTGAG ATTCGAGGT ACAGGACCCG

801 CTAAAATCGT ATAAAATCTG GATTTTTTTN TTTTTTTTTG CGCATATTCA
CATATGTAAA CCAGAACATT CTATGTACTA
GATTTTAGCA TATTTTAGAC CTAAAAAAN AAAAAAAAC GCGTATAAGT
GTATACATTT GGTCTTGTA GATACATGAT

881 CAAACCTGGT TTTTAAAAAG GAACTATGTT GCTATGAATT AACTTGTGT
CGTGCTGATA GGACAGACTG GATTTTTTCAT
GTTTGGACCA AAAATTTTTC CTTGATACAA CGATACTTAA TTTGAACACA
GCACGACTAT CCTGTCTGAC CTAAAAAGTA

-3

<-----

961 ATTTCTTATT AAAATTTCTG CCATTTAGAA GAAGAGAACT ACATTCATGG
TTTGGAAGAG ATAAACCTGA AAAGAAGAGT
TAAAGAATAA TTTTAAAGAC GGTAAATCTT CTTCTCTTGA TGTAAGTACC
AAACCTTCTC TATTTGGACT TTTCTTCTCA

-3

1041 GGCCTTATCT TCACTTTATC GATAAGTCAG TTTATTTGTT TCATTGTGTA
CATTTTTATA TTCTCCTTTT GACATTATAA
CCGGAATAGA AGTGAAATAG CTATTCAGTC AAATAAACAA AGTAACACAT
GTAAAAATAT AAGAGGAAAA CTGTAATATT

-3

----- [

1121 CTGTTGGCTT TTCTAATCTT GTTAAATATA TCTATTTTTA CCAAAGGTAT
TTAATATTCT TTTTATGAC AACTTAGATC
GACAACCGAA AAGATTAGAA CAATTTATAT AGATAAAAAT GGTTTCCATA
AATTATAAGA AAAAATACTG TTGAATCTAG

1201 AACTATTTTT AGCTTGGTAA ATTTTTCTAA ACACAATTGT TATAGCCAGA
GGAACAAAGA TGATATAAAA TATTGTTGCT
TTGATAAAAA TCGAACCATT TAAAAAGATT TGTGTTAACA ATATCGGTCT
CCTTGTTTCT ACTATATTTT ATAACAACGA

1281 CTGACAAAAA TACATGTATT TCATTCTCGT ATGGTGCTAG AGTTAGATTA
ATCTGCATTT TAAAAAACTG AATTGGAATA
GACTGTTTTT ATGTACATAA AGTAAGAGCA TACCACGATC TCAATCTAAT
TAGACGTAAA ATTTTTTGAC TTAACCTTAT

1361 GAATTGGTAA GTTGCAAAGA CTTTTTGAAA ATAATTAAAT TATCATATCT
TCCATTCCCTG TTATTGGAGA TGAAAATAAA
CTTAACCATT CAACGTTTCT GAAAACTTT TATTAATTTA ATAGTATAGA
AGGTAAGGAC AATAACCTCT ACTTTTATTT

1441 AAGCAACTTA TGAAAGTAGA CATTCAGATC CAGCCATTAC TAACCTATTC
CTTTTTTGGG GAAATCTGAG CCTAGCTCAG
TTCGTTGAAT ACTTTCATCT GTAAGTCTAG GTCGGTAATG ATTGGATAAG
GAAAAAACCCT CTTTAGACTC GGATCGAGTC

32/54

FIG. 18 (CONTINUED 3).

1521 AAAACATAA AGCACCTTGA AAAAGACTTG GCAGCTTCCT GATAAAGCGT
GCTGTGCTGT GCAGTAGGAA CACATCCTAT
TTTTTGTATT TCGTGGAAC TTTTCTGAAC CGTCGAAGGA CTATTTGCA
CGACACGACA CGTCATCCTT GTGTAGGATA

1601 TTATTGTGAT GTTGTGGTTT TATTATCTTA AACTCTGTTC CATACTTG
TATAAATACA TGGATATTTT TATGTACAGA
AATAACACTA CAACACCAA ATAATAGAAT TTGAGACAAG GTATGTGAAC
ATATTTATGT ACCTATAAAA ATACATGTCT

1681 AGTATGTCTC TTAACCAGTT CACTTATTGT ACCTGG
TCATACAGAG AATTGGTCAA GTGAATAACA TGGACC

FIG. 19. DNA and polypeptide sequence used for mammalian cell expression 33/54

```

+1      m s l f g l l l l t s a l a g q r
1  GGATCCAAAA TGAGCCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC CGGCCAGAGA

+1  q g t q a E S N L S S K F Q F S S N K E
61  CAGGGGACTC AGGCGGAATC CAACCTGAGT AGTAAATTCC AGTTTTCCAG CAACAAGGAA

+1  Q N G V Q D P Q H E R I I T V S T N G S
121 CAGAACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA CTGTGTCTAC TAATGGAAGT

+1  I H S P R F P H T Y P R N T V L V W R L
181 ATTACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA CGGTCTTGGT ATGGAGATTA

+1  V A V E E N V W I Q L T F D E R F G L E
241 GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG ATGAAAGATT TGGGCTTGAA

+1  D P E D D I C K Y D F V E V E E P S D G
301 GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG TTGAGGAACC CAGTGATGGA

+1  T I L G R W C G S G T V P G K Q I S K G
361 ACTATATTAG GGCCCTGGTG TGGTTCTGGT ACTGTACCAG GAAAACAGAT TTCTAAAGGA

+1  N Q I R I R F V S D E Y F P S E P G F C
421 AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC CTTCTGAACC AGGGTCTGTC

+1  I H Y N I V M P Q F T E A V S P S V L P
481 ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG TGATCCTTC AGTGCTACCC

+1  P S A L P L D L L N N A I T A F S T L E
541 CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA CTGCCTTTAG TACCTTGGA

+1  D L I R Y L E P E R W Q L D L E D L Y R
601 GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCASTGG ACTTAAAGA TCTATATAGG

+1  P T W Q L L G K A F V F G R K S R V V D
661 CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTTGGAA GAAATCCAG AGTGGTGGAT

+1  L N L L T E E V R L Y S C T P R N F S V
721 CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA CACCTCGTAA CTTCTCAGTG

+1  S I R E E L K R T D T I F W P G C L L V
781 TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT GGCCAGGTTG TCTCCTGGTT

+1  K R C G G N C A C C L H N C N E C Q C V
841 AAACGCTGTG GTGGAAGCTG TGCCTGTTGT CTCCACAATT GCAATGAATG TCAATGTGTC

+1  P S K V T K K Y H E V L Q L R P K T G V
901 CCAAGCAAAG TTAATAAAAA ATACCACGAG GTCTTTCAGT TGAGACCAA GACCGGTGTC

+1  R G L H K S L T D V A L E H H E E C D C
961 AGGGGATTGC ACAATCACT CACCGACGTG GCCCTGGAGC ACCATGAGGA GTGTGACTGT

+1  V C R G S T G G S R G P F E G K P I P N
1021 GTGTGCAGAG GGAGACAGG AGGATCTAGA GGGCCCTTGG AAGGTAGCC TATCCCTAAC

+1  P L L G L D S T R T G H H H H H H
1081 CCTCTCCTCG GTCTCGATTC TACGCGTACC GGTGATGTC ACCATCACCA TTGA

```

FIG. 20. DNA and polypeptide sequence used for baculovirus/insect cell expression ^{34/54}

1 GAATTCAAAG GCTGTATTT TACTGTTTTT GTAACAGTTT TGTAATAAAA AAACCTATAA
 +3 m k f l v n v a l v f m v v y i s y i
 61 ATATGAAATT CTTAGTCAAC GTTGCCCTTG TTTTATGGT CGTATACATT TCTTACATCT
 +3 y a D P E S H H H H H H E S N L S S K F
 121 ATGCGGATCC CGAGTCTCAC CATCACCACC ATCATGAATC CAACCTGAGT AGTAAATTCC
 +3 Q F S S N K E Q N G V Q D P Q H E R I I
 181 AGTTTTCAG CAACAAGGAA CAGAACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA
 +3 T V S T N G S I H S P R F P H T Y P R N
 241 CTGTGTCTAC TAATGGAAGT ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA
 +3 T V L V W R L V A V E E N V W I Q L T F
 301 CGGTCTTGGT ATGAGATTA GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG
 +3 D E R F G L E D P E D D I C K Y D F V E
 361 ATGAAAGATT TGGGCTTGAA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG
 +3 V E E P S D G T I L G R W C G S G T V P
 421 TTGAGGAACC CAGTGATGGA ACTATATTAG GCGCTGGTG TGGTTCTGGT ACTGTACCAG
 +3 G K Q I S K G N Q I R I R F V S D E Y F
 481 GAAAACAGAT TTCTAAAGGA AATCAATTA GGATAAGATT TGTATCTGAT GAATATTTTC
 +3 P S E P G F C I H Y N I V M P Q F T E A
 541 CTTCTGAACC AGGTTCTGC ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG
 +3 V S P S V L P P S A L P L D L L N N A I
 601 TGAGTCCTTC AGTCTACCC CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA
 +3 T A F S T L E D L I R Y L E P E R W Q L
 661 CTGCCCTTAG TACCTTGGA GACCTTATTC CATATCTTGA ACCAGAGAGA TGGCAGTTGG
 +3 D L E D L Y R P T W Q L L G K A F V F G
 721 ACTTAGAAGA TCTATATAGG CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTGGAA
 +3 R K S R V V D L N L L T E E V R L Y S C
 781 GAAAATCCAG AGTGTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA
 +3 T P R N F S V S I R E E L K R T D T I F
 841 CACCTCGTAA CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT
 +3 W P G C L L V K R C G G N C A C C L H N
 901 GGCCAGGTTG TCTCTGGTT AAACGCTGTG GTGGGAAGTG TGCTGTTGT CTCCACAATT
 +3 C N E C Q C V P S K V T K K Y H E V L Q
 961 GCAATGAATG TCAATGTGTC CCAAGCAAAG TTAATAAAAA ATACCACGAG GTCCTTCAGT
 +3 L R P K T G V R G L H K S L T D V A L E
 1021 TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC
 +3 H H E E S D C V C R G S T G G
 1081 ACCATCAGGA GTGTACTGT GTGTGAGAG GGAGCACAGG AGGATAGCTC TAGA

FIG. 21. DNA and polypeptide sequence used for *E. coli* expression

35/54

+3 Q T N S S S N N N N N N N N N L G I
 1 CGCAGACTAA TTCGAGCTCG AACAAACAACA ACAATAACAA TAACAACAAC CTCGGGATCG

 +3 E G R I S E F E S N L S S K F Q F S S N
 61 AGGGAAGGAT TTCAGAATTC GAATCCAACC TGAGTAGTAA ATTCCAGTTT TCCAGCAACA

 +3 K E Q N G V Q D P Q H E R I I T V S T N
 121 AGGAACAGAA CGGAGTACAA GATCCTCAGC ATGAGAGAAT TATTACTGTG TCTACTAATG

 +3 G S I H S P R F P H T Y P R N T V L V W
 181 GAAGTATTCA CAGCCCAAGG TTTCCTCATA CTTATCCAAG AAATACGGTC TTGGTATGGA

 +3 R L V A V E E N V W I Q L T F D E R F G
 241 GATTAGTAGC AGTAGAGGAA AATGTATGGA TACAACCTAC GTTGATGAA AGATTGGGGC

 +3 L E D P E D D I C K Y D F V E V E E P S
 301 TTGAAGACCC AGAAGATGAC ATATGCAAGT ATGATTTTGT AGAAGTTGAG GAACCCAGTG

 +3 D G T I L G R W C G S G T V P G K Q I S
 361 ATGGAACTAT ATTAGGGCGC TGGTGTGGTT CTGGTACTGT ACCAGGAAAA CAGATTTCTA

 +3 K G N Q I R I R F V S D E Y F P S E P G
 421 AAGGAAATCA AATTAGGATA AGATTTGTAT CTGATGAATA TTTTCCTTCT GAACCAGGGT

 +3 F C I H Y N I V M P Q F T E A V S P S V
 481 TCTGCATCCA CTACAACATT GTCATGCCAC AATTCACAGA AGCTGTGAGT CCTTCAGTGC

 +3 L P P S A L P L D L L N N A I T A F S T
 541 TACCCCTTC AGCTTTGCCA CTGGACCTGC TTAATAATGC TATAACTGCC TTTAGTACCT

 +3 L E D L I R Y L E P E R W Q L D L E D L
 601 TGAAGACCT TATTCGATAT CTTGAACCAG ACAGATGGCA GTTGGACTTA GAAGATCTAT

 +3 Y R P T W Q L L G K A F V F G R K S R V
 661 ATAGGCCAAC TTGGCAACTT CTTGGCAAGG CTTTGTGTTT TGAAGAAAA TCCAGAGTGG

 +3 V D L N L L T E E V R L Y S C T P R N F
 721 TGGATCTGAA CCTTCTAACA GAGGAGGTAA GATTATACAG CTGCACACCT CGTAACTTCT

 +3 S V S I R E E L K R T D T I F W P G C L
 781 CAGTGTCCAT AAGGGAAGAA CTAAAGAGAA CCGATACCAT TTTCTGGCCA GGTGTCTCC

 +3 L V K R C G G N C A C C L H N C N E C Q
 841 TGGTTAAACG CTGTGGTGGG AACTGTGCCT GTTGTCTCCA CAATTGCAAT GAATGTCAAT

 +3 C V F S K V T K K Y H E V L Q L R P K T
 901 GTGTCCCAAG CAAAGTTACT AAAAAATACC ACGAGGTCTT TCAGTTGAGA CCAAGACCG

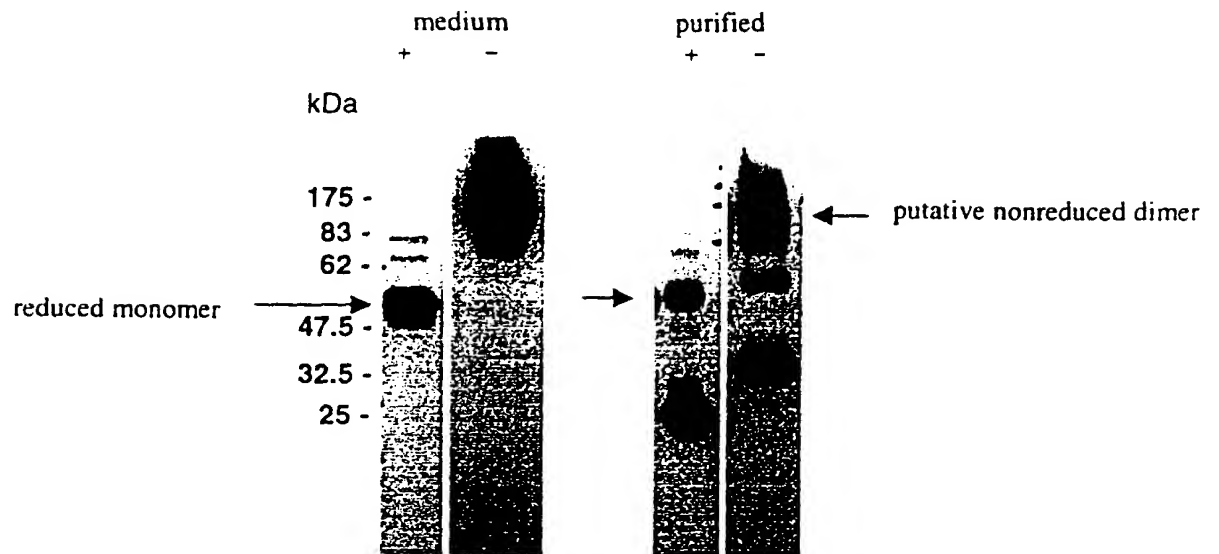
 +3 G V R G L H K S L T D V A L E H H E E C
 961 GTGTCAAGGG ATTGCACAAA TCACTCACCG ACGTGGCCCT GGAGCACCAT GAGGAGTGTG

 +3 D C V C R G S T G G H H H H H H H *
 1021 ACTGTGTGTG CAGAGGGAGC ACAGGAGGAC ATCATCACCA TCACCATTGA TCTAGAGTGC

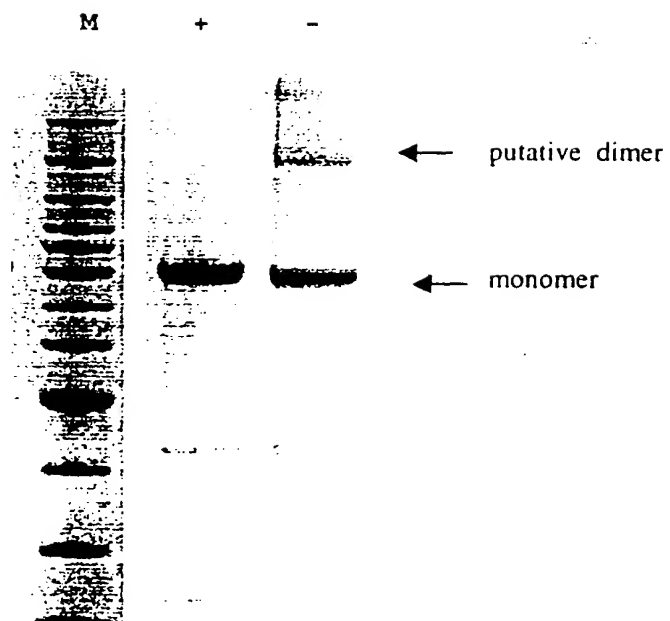
 1081 ACCTGTAGGC AAGCTT

36/54
FIG. 22. Disulphide-linked dimerisation of VEGF-X

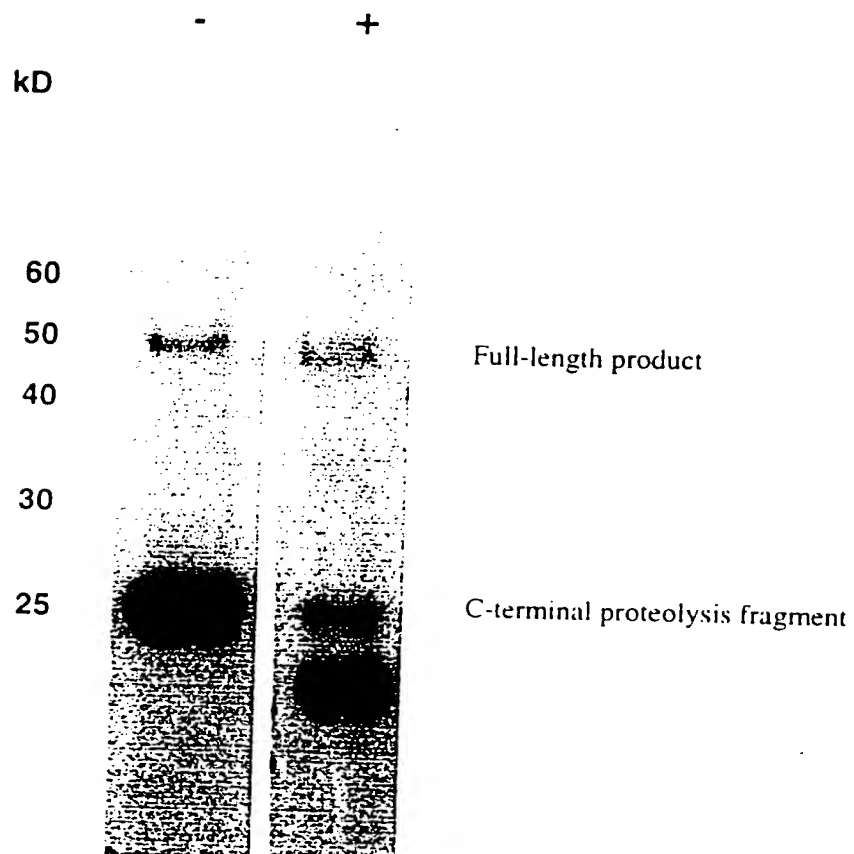
(A) Mammalian cell expression



(B) *E.coli* expression



37/54

FIG. 23. Glycosylation of VEGF-X

38/54

FIG. 24.

DNA and polypeptide sequence used for *E.coli* expression of the PDGF-like domain

```

+3      M R G S H H H H H H G M A S M
1  AAGGAGATAT ACATATGCGG GGTTCATC ATCATCATCA TCATGGTATG GCTAGCATGA

+3  T G G O Q M G R D L Y D D D D K D P G R
61 CTGGTGGACA GCAAATGGGT CGGGATCTGT ACGACGATGA CGATAAGGAT CCGGGAAGAA

+3  K S R V V D L N L L T E E V R L Y S C T
121 AATCCAGAGT GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC

+3  P R N F S V S I R E E L K R T D T I F W
181 CTCGTAACTT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATAACC ATTTTCTGGC

+3  P G C L L V K R C G G N C A C C L H N C
241 CAGGTGTCTC CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA

+3  N E C Q C V P S K V T K K Y H E V L Q L
301 ATGAATGTCA ATGTGTCCCA AGCAAAGTTA CTAAAAAATA CCACGAGGTC CTTCAGTTGA

+3  R P K T G V R G L H K S L T D V A L E H
361 GACCAAAGAC CCGTGTGAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGAGCACC

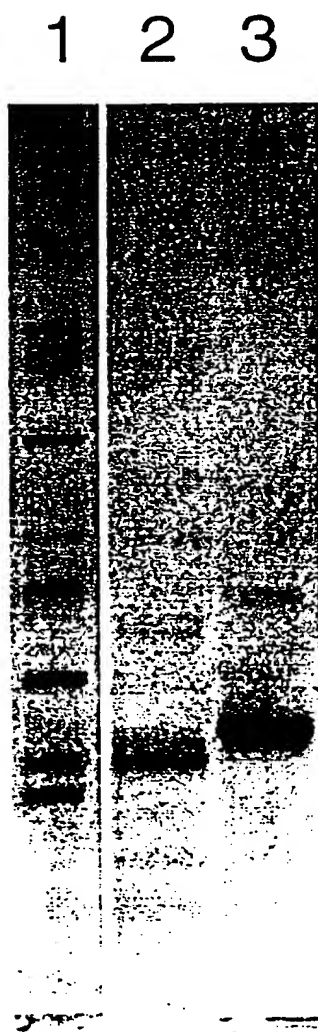
+3  H E E C D C V C R G S T G G
421 ATGAGGAGTG TCACTGTGTG TGCAGAGGGA GCACAGGAGG ATAATGAATT CGAAGCTTGA

481 TCCGGCTGCT AACAAAGCCC

```

39/54

FIG. 25. Expression of PDGF domain in *E.coli*



40/54

FIG. 26.

DNA and polypeptide sequence used for *E.coli* expression of the CUB-like domain

```

+2   M A M D I G I N S D P E S H H H H H H
1   G G C G A T G G C C A T G G A T A T C G A A T T A A T T C G G A T C C G G A G T C T C A C C A T C A C C A C C A T C A

+2   E S N L S S K F Q F S S N K E Q N G V Q
61  T G A A T C C A A C C T G A G T A G T A A A T T C C A G T T T T C C A G C A A C A A G G A A C A G A A C G G A G T A C A

+2   D P Q H E R I I T V S T N G S I H S P R
121 A G A T C C T C A G C A T G A G A G A A T T A T T A C T G T G T C T A C T A A T G G A A G T A T T C A C A G C C C A A G

+2   F P H T Y P R N T V L V W R L V A V E E
181 G T T C C T C A T A C T A T C C A A G A A T A C G G T C T G G T A T G G A G A T T A G T A G C A G T A G A G G A

+2   N V W I Q L T F D E R F G L E D P E D D
241 A A A T G T A T G G A T A C A A C T T A C G T T G A T G A A A G A T T T G G G C T T G A A G A C C C A G A A G A T G A

+2   I C K Y D F V E V E E P S D G T I L G R
301 C A T A T G C A A G T A T G A T T T T G T A G A A G T T G A G G A C C C A S T G A T G G A A C T A T A T T A G G G C G

+2   W C G S G T V P G K Q I S K G N Q I R I
361 C T G G T G T G G T T C T G G T A C T G T A C C A G G A A A C A G A T T T C T A A G G A A A T C A A A T T A G G A T

+2   R F V S D E Y F P S E P G F C I H Y N I
421 A A G A T T T G T A T C T G A T G A A T A T T T C C T T C T G A A C C A G G T T C T G C A T C C A C T A C A A C A T

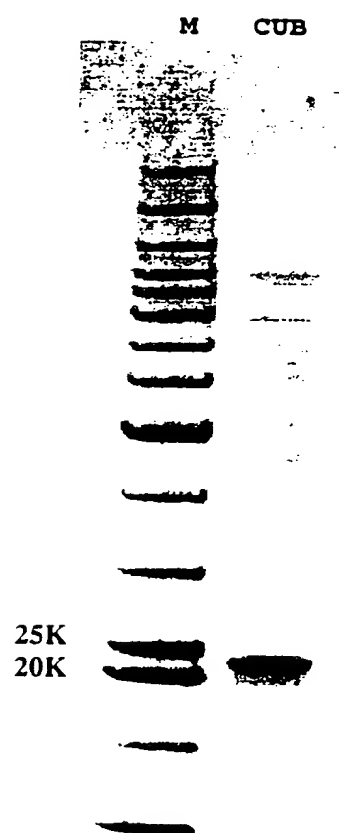
+2   V M P C F T E A V
491 T G T C A T G C C A C A A T T C A C A G A A G C T G T G T A G T C G A G C T C C G T C G A C A A G C T T G C G G C C G C

541 A C T C G A G C A C

```

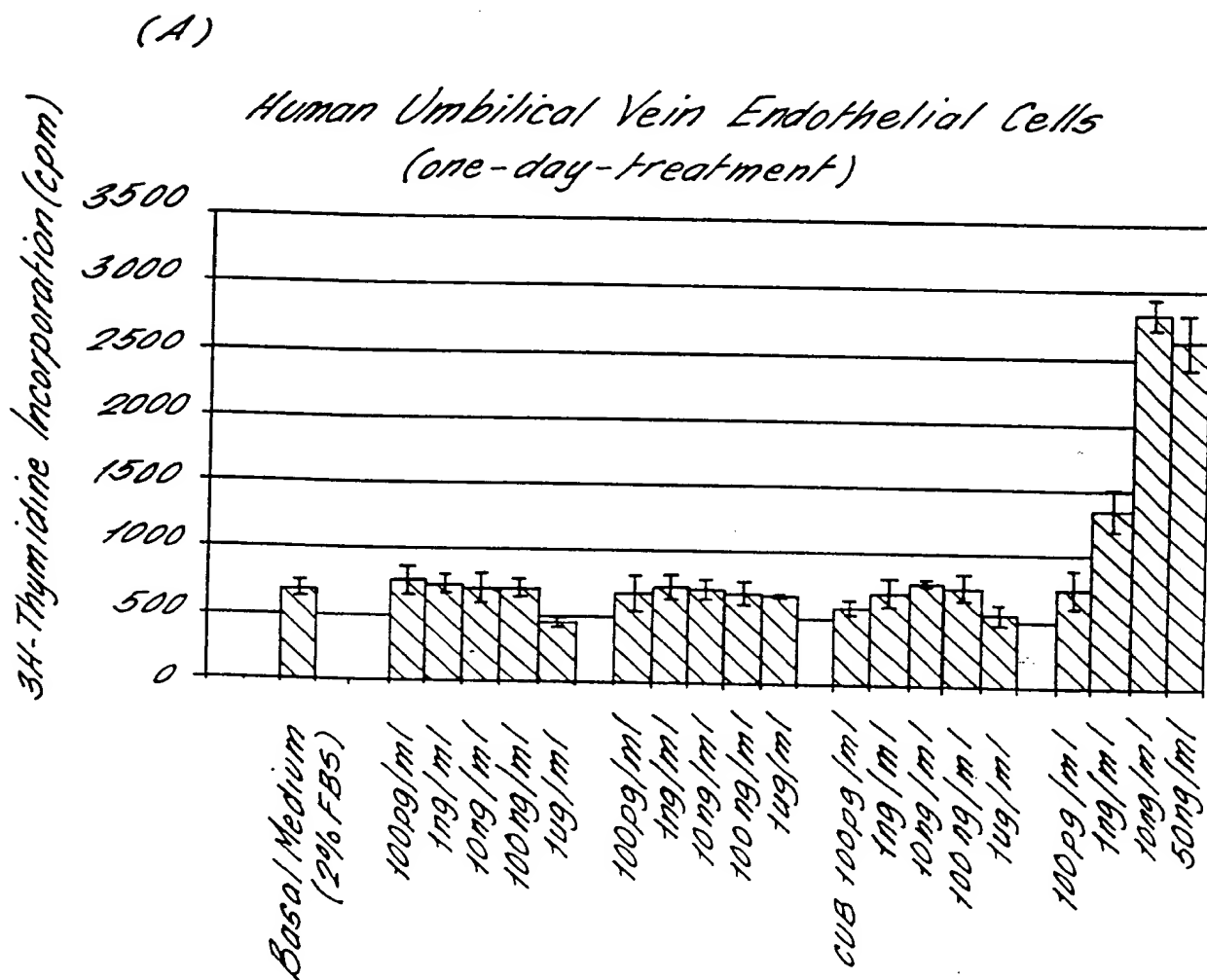

41/54

FIG. 27. Expression of the CUB domain in *E.coli*



42/54

FIG. 28. The Effect of Truncated VEGF-X (CUB domain) on HUVEC Proliferation.

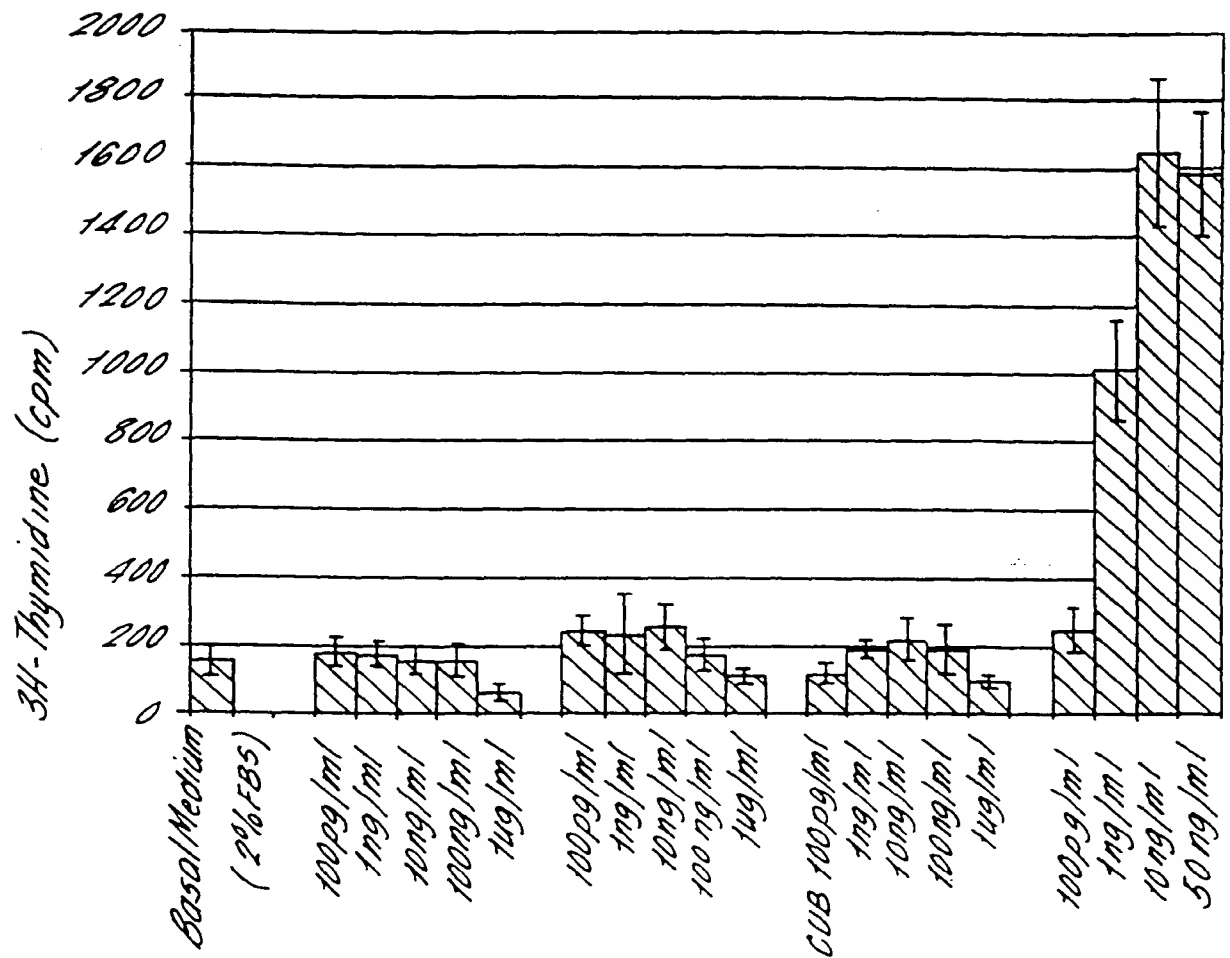


43/54

FIG. 28 (CONTINUED 1).

(8)

Human Umbilical Vein Endothelial Cells (24-hour-starving Followed by one-day-treatment)



44/54

FIG. 28 (CONTINUED 2).

(C)

The effect of VEGF-A₁₆₅ and VEGF-X CUB domain on the proliferation of HUVEC (two-day-treatment).

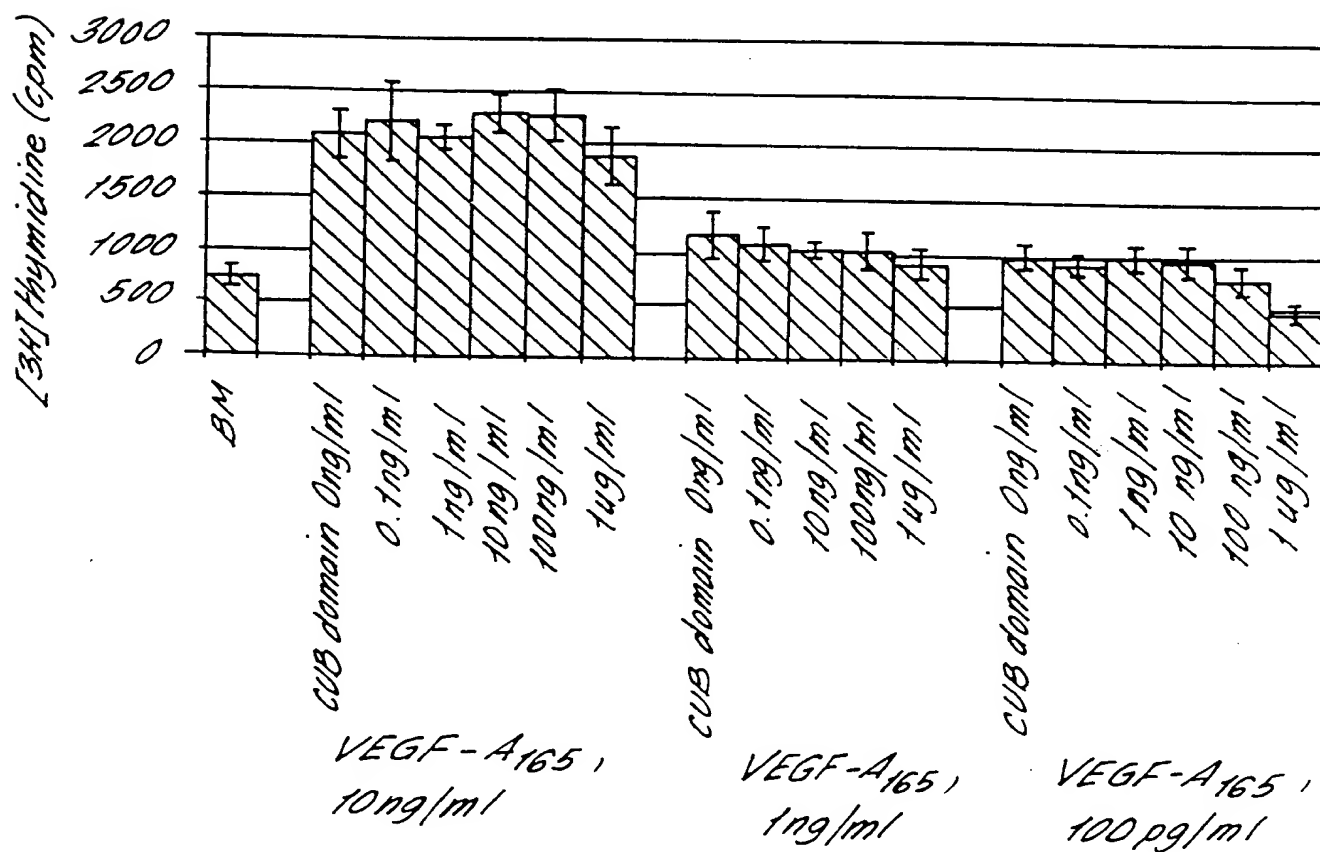


FIG. 29.

Tissue distribution of mRNA

(A) - Normal tissues

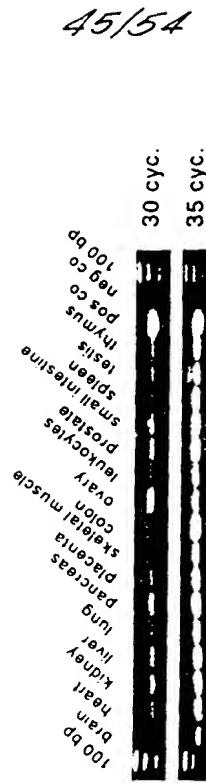
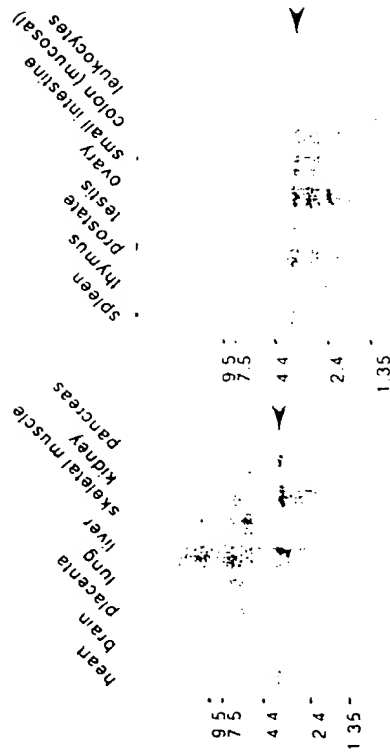
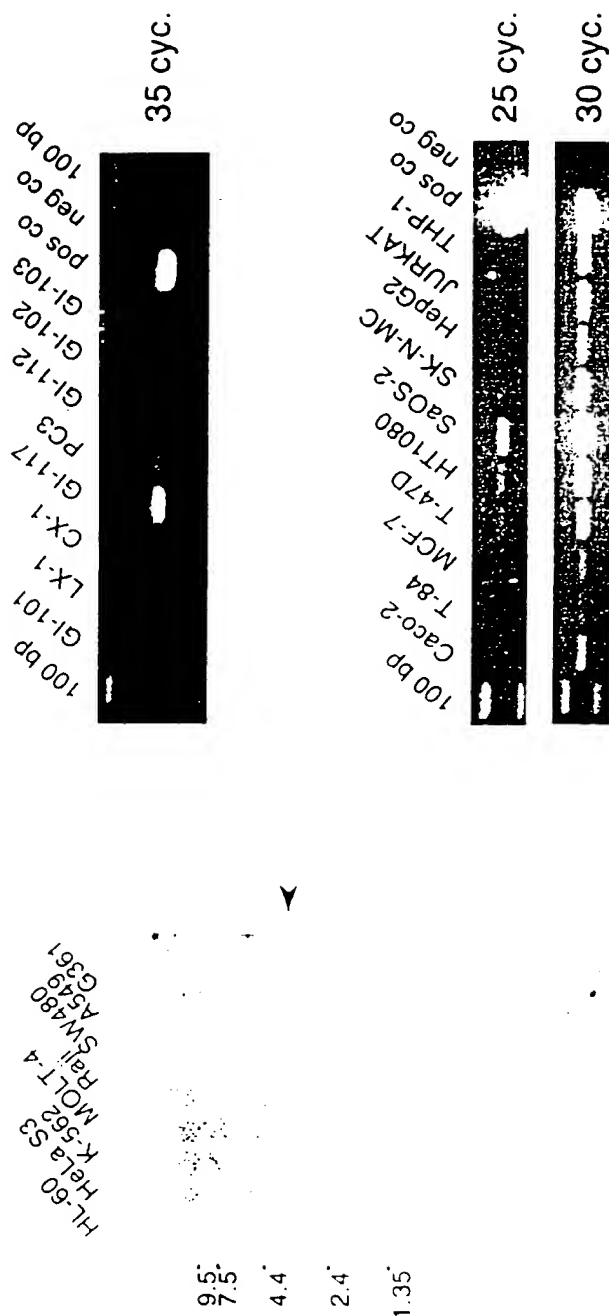


FIG. 29 (CONTINUED). (B)- Tumour tissue and cell lines



47/54

FIG. 30.

Partial intron/exon structure of the VEGF-X gene

(A) - Genomic DNA sequences of 2 exons determined by sequencing

tttctttttataccatatagtggtggatctgaaccagGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAGAAGCTGTG
 AGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGGAAAGACCTTAT
 TCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAAGTTGGCAACTTCTTGGCAAGGCTTTTGT
 TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTG
 TCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAAGCTGTGCCTG
 TTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGtaggtatacaattttcttttt
 ggtttccttcgggtattttatg:cct

aaagccagtcatacacattcggtgatTTTTAAAGTGGCTTactcttatccctttcagGTCCTTCAGTTGAGACCAAAGACCGGT
 GTCAGGGGATTGCACAAATCACTACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGG
 ATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATCGCTTATCTCCAT
 CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAAATTAG
 GAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATT
 AAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTCGATACGGCTTAG
 GGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGGCTTAACTCTAAAGCTCCATGTCTGGGC
 CTAATAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGGCGCATATTCACATATGTAAACCAGAACATTCTATGTACTACAAACC
 TGGTTTTTAAAAAGGAAGTATGTTGCTATGAATTAACCTTGTGTGATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAA
 AATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTA
 TCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTATATCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTA
 AATATATCTATTTTACCAAAGGTATTTAATATCTTTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAATTTTCTAA
 ACACAATTGTTATAGCCAGAGGACAAAGATGATATAAAATATTGTTGCTGTGACAAAAATACATGTATTTCACTCTCGTATGGTG
 CTAGAGTTAGATTAACTGCAATTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAAGACTTTTGAATAAATTAAATTA
 TCATATCTTCCATTCTGTTATTGGAGATGAAAAATAAAAGCAACTTATGAAAGTAGACATTGAGATCCAGCCATTACTAACCTAT
 TCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAGAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTG
 TGCTGTGCAGTAGGAACACATCCTATTTATTGTGATGTTGTGGTTTTATTATCTTAACTCTGTTCCATACACTTGTATAAATACA
 TGGATATTTTTATGTACAGAAGTATGTCTCTTAACCAGTTCACTTATTGTACTCTGGCAATTTAAAGAAAAATCAGTAAAAATTT
 TGCTTGTAATAATGCTTAATATCGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAAATAAAGAAATG
 GGCTATTTTGGGGAGAAAATtatgctgctgctgctcaagatttatctctggactctgagaaaa:gaaagataaa

FIG. 30 (CONTINUED 1). 48/54

(B) - Location of splice sites within the cDNA sequence

1 GAATTCGCCC TTTTGTTTAA ACCTTGGGAA CTGGTTCAGG TCCAGGTTTT GCTTTGATCC
 61 TTTTCAAAAA CTGGAGACAC AGAAGAGGGC TCTAGGAAAA AGTTTTGGAT GGGATTATGT
 121 GGAAACTACC CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCAC CCCAGTGCAG
 181 CCTTCCCCTG GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCCCGCTG
 +3 M S L F G L L L L T S
 241 AGTGAGCTCT CACCCCACTC AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG
 +3 A L A G Q R Q G T Q A E S N L S S K F Q
 301 CCCTGGCCGG CCAGAGACAG GGGACTCAGG CGGAATCCAA CCTGAGTAGT AAATCCAGT
 +3 F S S N K E Q N G V Q D P Q H E R I I T
 361 TTTCCAGCAA CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG
 +3 V S T N G S I H S P R F P H T Y P R N T
 421 TGTCTACTAA TGGAAGTATT CACAGCCCAA GGTTCCTCA TACTTATCCA AGAAATACGG
 +3 V L V W R L V A V E E N V W I Q L T F D
 481 TCTTGGTATG GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACAACTT ACGTTTGATG
 +3 E R F G L E D P E D D I C K Y D F V E V
 541 AAAGATTTGG GCTTGAAGAC CCAGAAGATG ACATATGCAA GTATGATTTT GTASAASTTG
 +3 E E P S D G T I L G R W C G S G T V P G
 601 AGGAACCCAG TGATGGAAT ATATTAGGGC GCTGGTGTGG TTCTGGTACT GTACCAGGAA
 +3 K Q I S K G N Q I R I R F V S D E Y F P
 661 AACAGATTTT TAAAGGAAAT CAAATTAGGA TAAGATTTGT ATCTGATGAA TATTTTCCTT
 +3 S E P | G F C I H Y N I V M P Q F T E A V
 721 CTGAACCAAG GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTCACA GAAGCTGTGA
 +3 S P S V L P P S A L P L D L L N N A I T
 781 GTCCTTCAGT GCTACCCCTC TCAGCTTTGC CACTGGACCT GCTTAATAAT GCTATAACTG
 +3 A F S T L E D L I R Y L E P E R W Q L D
 841 CCTTTAGTAC CTGGAAGAC CTTATTCGAT ATCTTGAACC AGAGAGATGG CASTTGGACT
 +3 L E D L Y R P T W Q L L G K A F V F G R
 901 TAGAAGATCT ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTTGTG TTTGGAAGAA
 +3 K S R V V D L N L L T E E / R L Y S C T
 961 AATCCAGAGT GGTGGATCTG AACTTTCTAA CAGAGGAGT AAGATTATAC AGCTGCACAC
 +3 P R N F S V S I R E E L K R T D T I F W
 1021 CTCGTAACCT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC
 +3 P G C L L V K R C G G N C A C C L H N C
 1081 CAGGTTGTCT CCTGGTTAAA CCTGTGGTGG GGAAGTGTCC CTGTTGTCTC CACAATTCGA
 +3 N E C Q C V P S K V T K K Y H E | V L Q L

49/54

FIG. 30 (CONTINUED 2).

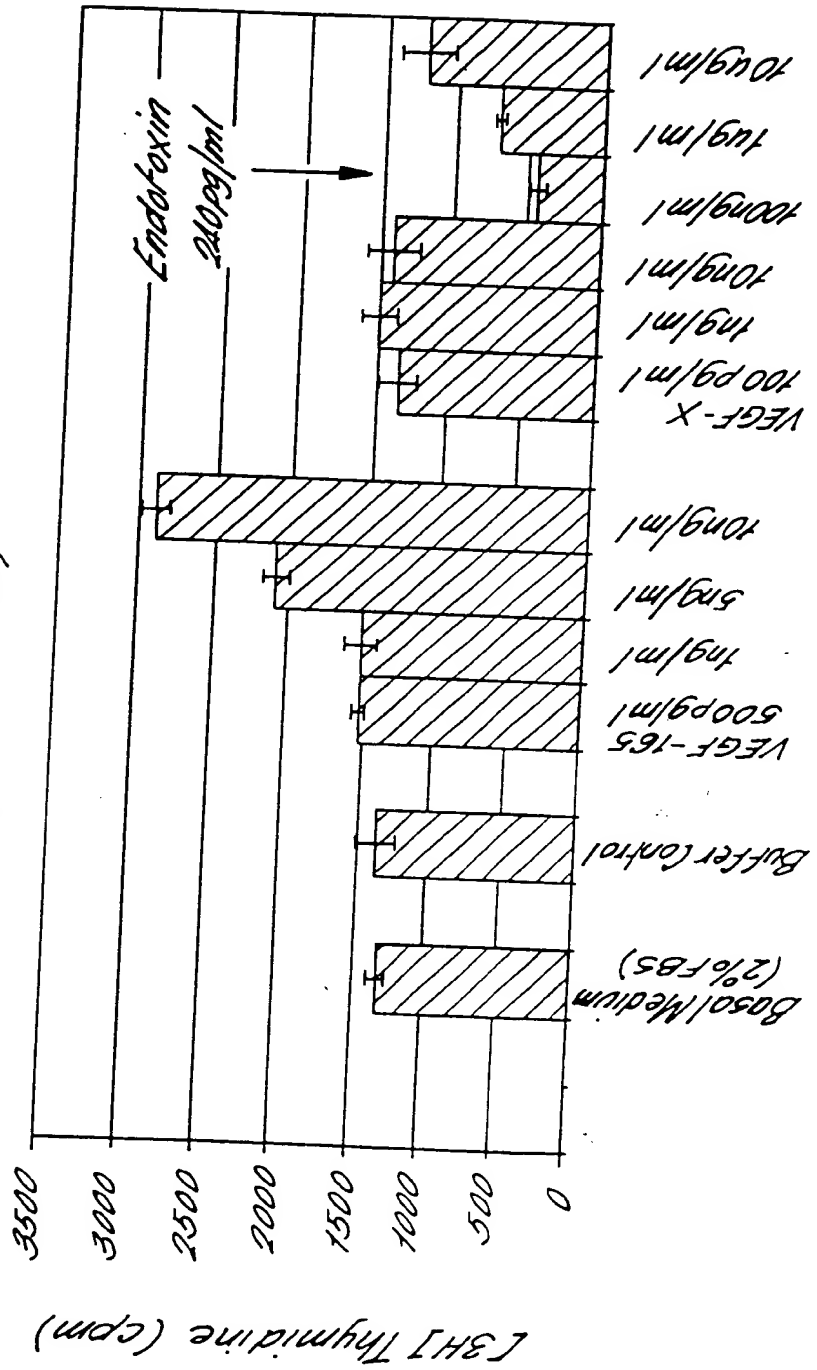
+3 R P K T G V R G L H K S L T D V A L E H
 1201 GACCAAAGAC CCGTGTG CAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC

 +3 H E E C D C V C R G S T G G
 1261 ATGAGGAGTG TCACTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC
 1321 AGCTCTTGCC CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT
 1381 CTCCATCCTT AATCTCAGTT GTTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC
 1441 ATTCTGAAAG AGGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT TTTGAGAGGA
 1501 GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAAG AAAATTAAAT GTTGTATTAA
 1561 ATAGATCACC AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTTCGTAT
 1621 TTCAGTTCTT TCGATACGGC TTAGGGTAAT GTCAGTACAG GAAAAAACT GTGCAAGTGA
 1681 GCACCTGATT CCGTGCCTT GCTTAACTCT AAAGCTCCAT GTCCTGGGCC TAAAATCGTA
 1741 TAAAATCTGG ATTTTTTTTT TTTTTTTTG CTCATATTCA CATATGAAA CCAGAACATT
 1801 CTATGTACTA CAAACCTGGT TTTTAAAAAG GAACTATGTT GCTATGAATT AAACCTGTGT
 1861 CATGCTGATA GGACAGACTG GATTTTTTCAT ATTTCTTATT AAAATTTCTG CCATTTAGAA
 1921 GAAGAGAACT ACATTCATGG TTTGGAAGAG ATAAACCTGA AAAGAAGAGT GGCCTTATCT
 1981 TCACTTTATC GATAAGTCAG TTTATTTGTT TCATTGTGTA CATTTTTATA TTCTCCTTTT
 2041 GACATTATAA CTGTTGGCTT TTCTAATCTT GTTAAATATA TCTATTTTTA CCAAAGGTAT
 2101 TTAATATTCT TTTTATGAC AACTTAGATC AACTATTTTT AGCTTGGTAA ATTTTCTAA
 2161 ACACAATTGT TATAGCCAGA GGAACAAAGA TGATATAAAA TATTGTTGCT CTGACAAAAA
 2221 TACATGTATT TCAITCTCGT ATGGTGCTAG AGTTAGATTA ATCTGCATTT TAAAAAAGT
 2281 AATTGGAATA GAATTGGTAA GTTGCAAAGA CTTTTGAAA ATAATTAAAT TATCATATCT
 2341 TCCATTCTTG TTAITGGAGA TGAAAATAAA AAGCAACTTA TGAAAGTAGA CATTGAGATC
 2401 CAGCCATTAC TAACCTATTC CTTTTTTGGG GAAATCTGAG CCTAGCTCAG AAAACATAA
 2461 AGCACCTTGA AAAAGACTTG GCAGCTTCCT GATAAAGCGT GCTGTGCTGT GCAGTAGGAA
 2521 CACATCCTAT TTAITGTGAT GTTGTGGTTT TATTATCTTA AACTCTGTTT CATACACTTG
 2581 TATAAATACA TCGATATTTT TATGTACAGA AGTATGTCTC TTAACCAGTT CACTTATTGT
 2641 ACCTGGAAGG CCGAATTCTG CAGATATC

50/54

FIG. 31.

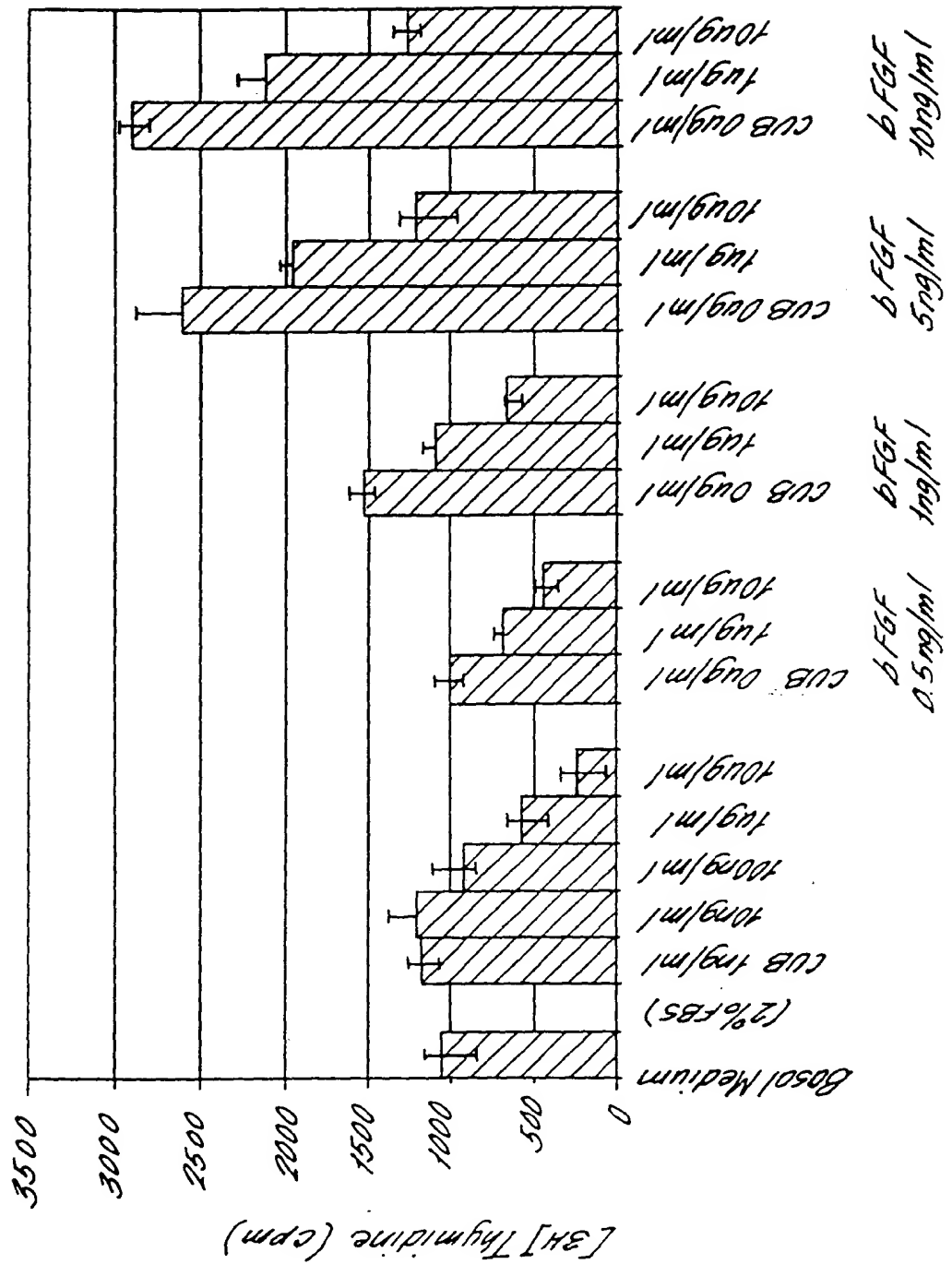
The Effect of Fl-VEGF-X on HUVEC Proliferation:
(24-hour serum starvation followed by
one day-treatment)



52/54

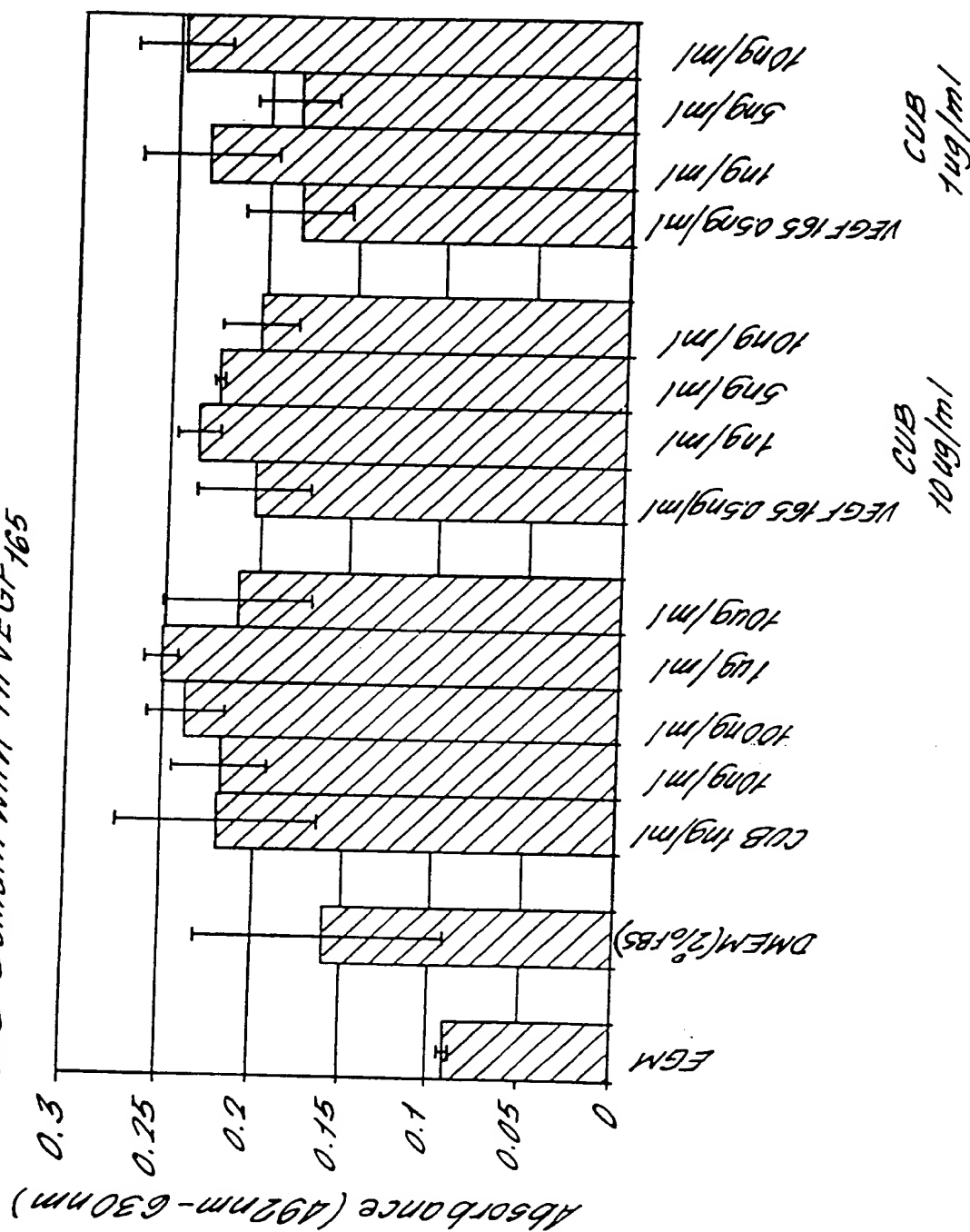
FIG. 33.

The Combined Effect of CUB Domain and Human Recombinant bFGF on HUVEC Proliferation: (24-hour serum starvation followed by two-day-treatment).



53/54

FIG. 34.
LDH Assay for Testing Cytotoxicity of CUB Domain or
CUB Domain with rh VEGF₁₆₅



54/54

FIG. 35.

LDH Assay for Testing Cytotoxicity of CUB Domain or
CUB Domain with rh-bFGF

